



SEQUENCE LISTING

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<120> METHODS AND MICROORGANISMS FOR PRODUCTION OF
PANTO-COMPOUNDS

<130> BGI-141CP

<140> USSN 09/667,569

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<160> 94

<170> PatentIn. Ver. 2.0

<210> 1

<211> 311

<212> PRT

<213> Haemophilus influenzae

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Met Glu Phe Ser Thr Gln Gln Thr Pro Phe Leu Ser Phe Asn Arg Glu
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Gln Trp Ala Glu Leu Arg Lys Ser Val Pro Leu Lys Leu Thr Glu Gln
20 25 30

Asp Leu Lys Pro Leu Leu Gly Phe Asn Glu Asp Leu Ser Leu Asp Glu
35 40 45

Val Ser Thr Ile Tyr Leu Pro Leu Thr Arg Leu Ile Asn Tyr Tyr Ile
50 55 60

Asp Glu Asn Leu His Arg Gln Thr Val Leu His Arg Phe Leu Gly Arg
65 70 75 80

Asn Asn Ala Lys Thr Pro Tyr Ile Ile Ser Ile Ala Gly Ser Val Ala
85 90 95

Val Gly Lys Ser Thr Ser Ala Arg Ile Leu Gln Ser Leu Leu Ser His
100 105 110

Trp Pro Thr His Arg Lys Val Asp Leu Ile Thr Thr Asp Gly Phe Leu
115 120 125

Tyr Pro Leu Asn Lys Leu Lys Gln Asp Asn Leu Leu Gln Lys Lys Gly
 130 131 140
 Phe Pro Val Ser Tyr Asp Thr Pro Lys Leu Ile Arg Phe Leu Ala Asp
 145 150 155 160
 Val Lys Ser Gly Lys Ser Asn Val Thr Ala Pro Ile Tyr Ser His Leu
 165 170 175
 Thr Tyr Asp Ile Ile Pro Asp Lys Phe Asp Val Val Asp Lys Pro Asp
 180 185 190
 Ile Leu Ile Leu Glu Gly Leu Asn Val Leu Gln Thr Gly Asn Asn Lys
 195 200 205
 Thr Asp Gln Thr Phe Val Ser Asp Phe Val Asp Phe Ser Ile Tyr Val
 210 215 220
 Asp Ala Glu Glu Lys Leu Leu Lys Glu Trp Tyr Ile Lys Arg Phe Leu
 225 230 235 240
 Lys Phe Arg Glu Ser Ala Phe Asn Asp Pro Asn Ser Tyr Phe Lys His
 245 250 255
 Tyr Ala Ser Leu Ser Lys Glu Glu Ala Ile Ala Thr Ala Ser Lys Ile
 260 265 270
 Trp Asp Glu Ile Asn Gly Leu Asn Leu Asn Gln Asn Ile Leu Pro Thr
 275 280 285
 Arg Glu Arg Ala Asn Leu Ile Leu Lys Lys Gly His Asn His Gln Val
 290 295 300
 Glu Leu Ile Lys Leu Arg Lys
 305 310

<210> 2
 <211> 316
 <212> PRT
 <213> Escherichia coli

<400> 2
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 Arg Asn Gln Trp Ala Ala Leu Arg Asp Ser Val Pro Met Thr Leu Ser
 20 25 30
 Glu Asp Glu Ile Ala Arg Leu Lys Gly Ile Asn Glu Asp Leu Ser Leu
 35 40 45
 Glu Glu Val Ala Glu Ile Tyr Leu Pro Leu Ser Arg Leu Leu Asn Phe
 50 55 60
 Tyr Ile Ser Ser Asn Leu Arg Arg Gln Ala Val Leu His Gln Phe Leu
 65 70 75 80
 N, Thr Asn Gly His Arg Ile Pro Tyr Ile Ile Ser Ile Ala Gly Ser
 85 90 95

Val Ala Val Gly Lys Ser Thr Thr Ala Arg Val Leu Gln Ala Leu Leu
 100 105 110
 Ser Arg Trp Pro Glu His Arg Arg Val Glu Leu Ile Thr Thr Asp Gly
 115 120 125
 Phe Leu His Pro Asn Gln Val Leu Lys Glu Arg Gly Leu Met Lys Lys
 130 135 140
 Lys Gly Phe Pro Glu Ser Tyr Asp Met His Arg Leu Val Lys Phe Val
 145 150 155 160
 Ser Asp Leu Lys Ser Gly Val Pro Asn Val Thr Ala Pro Val Tyr Ser
 165 170 175
 His Leu Ile Tyr Asp Val Ile Pro Asp Gly Asp Lys Thr Val Val Gln
 180 185 190
 Pro Asp Ile Leu Ile Leu Glu Gly Leu Asn Val Leu Gln Ser Gly Met
 195 200 205
 Asp Tyr Pro His Asp Pro His His Val Phe Val Ser Asp Phe Val Asp
 210 215 220
 Phe Ser Ile Tyr Val Asp Ala Pro Glu Asp Leu Leu Gln Thr Trp Tyr
 225 230 235 240
 Ile Asn Arg Phe Leu Lys Phe Arg Glu Gly Ala Phe Thr Asp Pro Asp
 245 250 255
 Ser Tyr Phe His Asn Tyr Ala Lys Leu Thr Lys Glu Glu Ala Ile Lys
 260 265 270
 Thr Ala Met Thr Leu Trp Lys Glu Ile Asn Trp Leu Asn Leu Lys Gln
 275 280 285
 Asn Ile Leu Pro Thr Arg Glu Arg Ala Ser Leu Ile Leu Thr Lys Ser
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 Ala Asn His Ala Val Glu Glu Val Arg Leu Arg Lys
 305 310 315

<210> 3
 <211> 319
 <212> FRT
 <213> *Bacillus subtilis*

400> 3
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 1 5 10
 Arg Glu Ser Trp Ser Gly Phe Gly Gly His Leu Ser Ile Ala Val Ser
 15 20 25
 Gln Gln Glu Ala Lys Ala Val Glu Gly Leu Asn Asp Tyr Leu Ser Val
 30 35 40
 Gln Gln Val Glu Thr Ile Tyr Ile Leu Val Arg Leu Leu His Leu
 45 50 55

His Val Lys Ser Ala Ala Glu Arg Asn Lys His Val Asn Val Phe Leu
 68 70 75 80
 Lys His Pro His Ser Ala Lys Ile Pro Phe Ile Ile Gly Ile Ala Gly
 85 90 95
 Ser Val Ala Val Gly Lys Ser Thr Thr Ala Arg Ile Leu Gln Lys Leu
 100 105 110
 Leu Ser Arg Leu Pro Asp Arg Pro Lys Val Ser Leu Ile Thr Thr Asp
 115 120 125
 Gly Phe Leu Phe Pro Thr Ala Glu Leu Lys Lys Lys Asn Met Met Ser
 130 135 140
 Arg Lys Gly Phe Pro Glu Ser Tyr Asp Val Lys Ala Leu Leu Glu Phe
 145 150 155 160
 Leu Asn Asp Leu Lys Ser Gly Lys Asp Ser Val Lys Ala Pro Val Tyr
 165 170 175
 Ser His Leu Thr Tyr Asp Arg Glu Glu Gly Val Phe Glu Val Val Glu
 180 185 190
 Gln Ala Asp Ile Val Ile Ile Glu Gly Ile Asn Val Leu Gln Ser Pro
 195 200 205
 Thr Leu Glu Asp Asp Arg Glu Asn Pro Arg Ile Phe Val Ser Asp Phe
 210 215 220
 Phe Asp Phe Ser Ile Tyr Val Asp Ala Glu Glu Ser Arg Ile Phe Thr
 225 230 235 240
 Trp Tyr Leu Glu Arg Phe Arg Leu Leu Arg Glu Thr Ala Phe Gln Asn
 245 250 255
 Pro Asp Ser Tyr Phe His Lys Phe Lys Asp Leu Ser Asp Gln Glu Ala
 260 265 270
 Asp Glu Met Ala Ala Ser Ile Trp Glu Ser Val Asn Arg Pro Asn Leu
 275 280 285
 Tyr Glu Asn Ile Leu Pro Thr Lys Phe Arg Ser Asp Leu Ile Leu Arg
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 Lys Gly Asp Gly His Lys Val Glu Glu Val Leu Val Arg Arg Val
 305 310 315

<010> 4

<011> 312

<012> FRT

<013> Mycobacterium leprae

<014> 4

Met Pro Arg Leu Ser Glu Pro Ser Pro Tyr Val Ala Phe Asp Arg Lys
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Ala Trp Arg Ala Leu Arg Met Ser Thr Pro Leu Ala Leu Thr Ala Ala
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Glu Leu Ile Gly Leu Arg Gly Leu Gly Glu Gln Ile Asp Leu Leu Glu
 35 40 45
 Val Glu Glu Val Tyr Leu Pro Leu Ala Arg Leu Ile His Leu Gln Val
 50 55 60
 Ala Ala Arg Gln Arg Leu Phe Ala Ala Thr Ala Glu Phe Leu Gly Glu
 65 70 75 80
 Pro Gln Gln Asn Pro Gly Arg Pro Val Pro Phe Ile Ile Gly Val Ala
 85 90 95
 Gly Ser Val Ala Val Gly Lys Ser Thr Thr Ala Arg Val Leu Gln Ala
 100 105 110
 Leu Leu Ala Arg Trp Asp His His Thr Arg Val Asp Leu Val Thr Thr
 115 120 125
 Asp Gly Phe Leu Tyr Pro Asn Ala Glu Leu Gly Arg Arg Asn Leu Met
 130 135 140
 His Arg Lys Gly Phe Pro Glu Ser Tyr Asn Arg Arg Ala Leu Met Arg
 145 150 155 160
 Phe Val Thr Ser Val Lys Ser Gly Ala Asp Tyr Ala Cys Ala Pro Val
 165 170 175
 Tyr Ser His Leu Arg Tyr Asp Thr Ile Pro Gly Ala Lys His Val Val
 180 185 190
 Arg His Pro Asp Ile Leu Ile Leu Glu Gly Leu Asn Val Leu Gln Thr
 195 200 205
 Gly Pro Thr Leu Met Val Ser Asp Leu Phe Asp Phe Ser Leu Tyr Val
 210 215 220
 Asp Ala Arg Ile Gln Asp Ile Glu Gln Trp Tyr Val Ser Arg Phe Leu
 225 230 235 240
 Ala Met Arg Gly Thr Ala Phe Ala Asp Pro Glu Ser His Phe His His
 245 250 255
 Tyr Ser Ala Leu Thr Asp Ser Lys Ala Ile Ile Ala Ala Arg Glu Ile
 260 265 270
 Trp Arg Ser Ile Asn Arg Pro Asn Leu Val Glu Asn Ile Leu Pro Thr
 275 280 285
 Arg Pro Arg Ala Thr Leu Val Leu Arg Lys Asp Ala Asp His Ser Ile
 290 295 300
 Asn Arg Leu Arg Leu Arg Lys Leu
 305 310

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Met Ser Arg Leu Ser Glu Pro Ser Pro Tyr Val Glu Phe Asp Arg Arg
 1 5 10 15
 Gln Trp Arg Ala Leu Arg Met Ser Thr Pro Leu Ala Leu Thr Glu Glu
 20 25 30
 Glu Leu Val Gly Leu Arg Gly Leu Gly Glu Gln Ile Asp Leu Leu Glu
 35 40 45
 Val Glu Glu Val Tyr Leu Pro Leu Ala Arg Leu Ile His Leu Gln Val
 50 55 60
 Ala Ala Arg Gln Arg Leu Phe Ala Ala Thr Ala Glu Phe Leu Gly Glu
 65 70 75 80
 Pro Gln Gln Asn Pro Asp Arg Pro Val Pro Phe Ile Ile Gly Val Ala
 85 90 95
 Gly Ser Val Ala Val Gly Lys Ser Thr Thr Ala Arg Val Leu Gln Ala
 100 105 110
 Leu Leu Ala Arg Trp Asp His His Pro Arg Val Asp Leu Val Thr Thr
 115 120 125
 Asp Gly Phe Leu Tyr Pro Asn Ala Glu Leu Gln Arg Arg Asn Leu Met
 130 135 140
 His Arg Lys Gly Phe Pro Glu Ser Tyr Asn Arg Arg Ala Leu Met Arg
 145 150 155 160
 Phe Val Thr Ser Val Lys Ser Gly Ser Asp Tyr Ala Cys Ala Pro Val
 165 170 175
 Tyr Ser His Leu His Tyr Asp Ile Ile Pro Gly Ala Glu Gln Val Val
 180 185 190
 Arg His Pro Asp Ile Leu Ile Leu Glu Gly Leu Asn Val Leu Gln Thr
 195 200 205
 Gly Pro Thr Leu Met Val Ser Asp Leu Phe Asp Phe Ser Leu Tyr Val
 210 215 220
 Asp Ala Arg Ile Glu Asp Ile Glu Gln Trp Tyr Val Ser Arg Phe Leu
 225 230 235 240
 Ala Met Arg Thr Thr Ala Phe Ala Asp Pro Glu Ser His Phe His His
 245 250 255
 Tyr Ala Ala Phe Ser Asp Ser Gln Ala Val Val Ala Ala Arg Glu Ile
 260 265 270
 Trp Arg Thr Ile Asn Arg Pro Asn Leu Val Glu Asn Ile Leu Pro Thr
 275 280 285
 Arg Pro Arg Ala Thr Leu Val Leu Arg Lys Asp Ala Asp His Ser Ile
 290 295 300
 Asn Arg Leu Arg Leu Arg Lys Leu
 305 310

<210> 6
 <211> 329
 <212> PRT
 <213> Streptomyces coelicolor

<400> 6
 Met Ile Ser Pro Val Pro Ser Ile Pro Arg Ser Ala His Arg Gln Arg
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 Pro Glu Ala Thr Pro Tyr Val Asp Leu Thr Arg Pro Glu Trp Ser Ala
 20 25 30
 Leu Arg Asp Lys Thr Pro Leu Pro Leu Thr Ala Glu Glu Val Glu Lys
 35 40 45
 Leu Arg Gly Leu Gly Asp Val Ile Asp Leu Asp Glu Val Arg Asp Ile
 50 55 60
 Tyr Leu Pro Leu Ser Arg Leu Leu Asn Leu Tyr Val Gly Ala Thr Asp
 65 70 75 80
 Gly Leu Arg Gly Ala Leu Asn Thr Phe Leu Gly Glu Gln Gly Ser Gln
 85 90 95
 Ser Gly Thr Pro Phe Val Ile Gly Val Ala Gly Ser Val Ala Val Gly
 100 105 110
 Lys Ser Thr Val Ala Arg Leu Leu Gln Ala Leu Leu Ser Arg Trp Pro
 115 120 125
 Glu His Pro Arg Val Glu Leu Val Thr Thr Asp Gly Phe Leu Leu Pro
 130 135 140
 Thr Arg Glu Leu Glu Ala Arg Gly Leu Met Ser Arg Lys Gly Phe Pro
 145 150 155 160
 Glu Ser Tyr Asp Arg Arg Ala Leu Thr Arg Phe Val Ala Asp Ile Lys
 165 170 175
 Ala Gly Lys Ala Glu Val Thr Ala Pro Val Tyr Ser His Leu Ile Tyr
 180 185 190
 Asp Ile Val Pro Asp Gln Arg Leu Val Val Arg Arg Pro Asp Ile Leu
 195 200 205
 Ile Val Glu Gly Leu Asn Val Leu Gln Pro Ala Leu Pro Gly Lys Asp
 210 215 220
 Gly Arg Thr Arg Val Gly Leu Ala Asp Tyr Phe Asp Phe Ser Val Tyr
 225 230 235 240
 Val Asp Ala Arg Thr Glu Asp Ile Glu Arg Trp Tyr Leu Asn Arg Phe
 245 250 255
 Arg Lys Leu Arg Ala Thr Ala Ile His Asn Pro Ser Ser Tyr Phe Arg
 260 265 270
 Lys Tyr Thr His Val Ser His His His Ala Leu Asp Tyr Ala Arg Thr
 275 280 285 290
 Thr Trp Arg Thr Ile Asn Tyr Leu Asn Leu Val Arg Asn Val Ala Pro

290

295

300

Thr Arg Gly Arg Ala Thr Leu Val Leu Arg Lys Gly Pro Asp His Lys
 305 310 315 320

Val Gln Arg Leu Ser Leu Arg Lys Leu
 325

<210> 7

<211> 265

<212> PRT

<213> Streptomyces coelicolor

<400> 7

Met Leu Leu Thr Ile Asp Val Gly Asn Thr His Thr Val Leu Gly Leu
 1 5 10 15

Phe Asp Gly Glu Asp Ile Val Glu His Trp Arg Ile Ser Thr Asp Ser
 20 25 30

Arg Arg Thr Ala Asp Glu Leu Ala Val Leu Leu Gln Gly Leu Met Gly
 35 40 45

Met His Pro Leu Leu Gly Asp Glu Leu Gly Asp Gly Ile Asp Gly Ile
 50 55 60

Ala Ile Cys Ala Thr Val Pro Ser Val Leu His Glu Leu Arg Glu Val
 65 70 75 80

Thr Arg Arg Tyr Tyr Gly Asp Val Pro Ala Val Leu Val Glu Pro Gly
 85 90 95

Val Lys Thr Gly Val Pro Ile Leu Thr Asp His Pro Lys Gln Val Gly
 100 105 110

Ala Asp Arg Ile Ile Asn Ala Val Ala Ala Val Glu Leu Tyr Gly Gly
 115 120 125

Pro Ala Ile Val Val Asp Phe Gly Thr Ala Thr Thr Phe Asp Ala Val
 130 135 140

Ser Ala Arg Gly Glu Tyr Ile Gly Gly Val Ile Ala Pro Gly Ile Glu
 145 150 155 160

Ile Ser Val Glu Ala Leu Gly Val Lys Gly Ala Gln Leu Arg Lys Ile
 165 170 175

Glu Val Ala Arg Pro Arg Ser Val Ile Gly Lys Asn Thr Val Glu Ala
 180 185 190

Met Gln Ser Gly Ile Val Tyr Gly Phe Ala Gly Gln Val Asp Gly Val
 195 200 205

Val Asn Arg Met Ala Arg Glu Leu Ala Asp Asp Phe Asp Asp Val Thr
 210 215 220

Val Ile Ala Thr Gly Gly Leu Ala Pro Met Val Leu Gly Glu Ser Ser
 225 230 235 240

Val Ile Asp Gln His Gln Pro Thr Leu Thr Leu Met Gly Leu Arg Leu

248

250

252

Val Tyr Glu Arg Asn Val Ser Arg Met
260 268

<210> 8

<211> 172

<212> BRT

<213> Mycobacterium tuberculosis

<400> 8

Met Leu Leu Ala Ile Asp Val Arg Asn Thr His Thr Val Val Gly Leu
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Leu Ser Gly Met Lys Glu His Ala Lys Val Val Gln Gln Trp Arg Ile
20 28 30

Arg Thr Glu Ser Glu Val Thr Ala Asp Glu Leu Ala Leu Thr Ile Asp
35 40 45

Gly Leu Ile Gly Glu Asp Ser Glu Arg Leu Thr Gly Thr Ala Ala Leu
50 55 60

Ser Thr Val Pro Ser Val Leu His Glu Val Arg Ile Met Leu Asp Gln
65 70 75 80

Tyr Trp Pro Ser Val Pro His Val Leu Ile Glu Pro Gly Val Arg Thr
85 90 95

Gly Ile Pro Leu Leu Val Asp Asn Pro Lys Glu Val Gly Ala Asp Arg
100 105 110

Ile Val Asn Cys Leu Ala Ala Tyr Asp Arg Phe Arg Lys Ala Ala Ile
115 120 125

Val Val Asp Phe Gly Ser Ser Ile Cys Val Asp Val Val Ser Ala Lys
130 135 140

Gly Glu Phe Leu Gly Gly Ala Ile Ala Pro Gly Val Gln Val Ser Ser
145 150 155 160

Asp Ala Ala Ala Ala Arg Ser Ala Ala Leu Arg Arg Val Glu Leu Ala
165 170 175

Arg Pro Arg Ser Val Val Gly Lys Asn Thr Val Gln Cys Met Gln Ala
180 185 190

Gly Ala Val Phe Gly Phe Ala Gly Leu Val Asp Gly Leu Val Gly Arg
195 200 205

Ile Arg Glu Asp Val Ser Gly Phe Ser Val Asp His Asp Val Ala Ile
210 215 220

Val Ala Thr Gly His Thr Ala Pro Leu Leu Leu Pro Glu Leu His Thr
225 230 235

Val Asp His Tyr Asp Gln His Leu Thr Leu Glu Gly Leu Arg Leu Val
240 245 250

Phe Gln Arg Asn Leu His Val His Arg Gly Arg Leu Lys Thr Ala Arg

180

185

200

<210> 2

<211> 15F

<212> PRT

<213> *Bacillus subtilis*

<400> 9

Leu Leu Leu Val Ile Asp Val Gly Asn Thr Asn Thr Val Leu Gly Val
 1 5 10 15

Tyr His Asp Gly Lys Leu Glu Tyr His Trp Arg Ile Glu Thr Ser Arg
 20 25 30

His Lys Thr Glu Asp Glu Phe Gly Met Ile Leu Arg Ser Leu Ile Asp
 35 40 45

His Ser Gly Leu Met Phe Glu Gln Ile Asp Gly Ile Ile Ile Ser Ser
 50 55 60

Val Val Pro Pro Ile Met Phe Ala Leu Glu Arg Met Cys Thr Lys Tyr
 65 70 75 80

Phe His Ile Glu Pro Gln Ile Val Gly Pro Gly Met Lys Thr Gly Leu
 85 90 95

Asn Ile Lys Tyr Asp Asn Pro Lys Glu Val Gly Ala Asp Arg Ile Val
 100 105 110

Asn Ala Val Ala Ala Ile His Leu Tyr Gly Asn Pro Leu Ile Val Val
 115 120 125

Asp Phe Gly Thr Ala Thr Thr Tyr Cys Tyr Ile Asp Glu Asn Lys Gln
 130 135 140

Tyr Met Gly Gly Ala Ile Ala Pro Gly Ile Thr Ile Ser Thr Glu Ala
 145 150 155 160

Leu Tyr Ser Arg Ala Ala Lys Leu Pro Arg Ile Glu Ile Thr Arg Pro
 165 170 175

Asp Asn Ile Ile Gly Lys Asn Thr Val Ser Ala Met Gln Ser Gly Ile
 180 185 190

Leu Phe Gly Tyr Val Gly Gln Val Glu Gly Ile Val Lys Arg Met Lys
 195 200 205

Trp Gln Ala Lys Gln Asp Leu Lys Val Ile Ala Thr Gly Gly Leu Ala
 210 215 220

Pro Leu Ile Ala Asn Gln Ser Asp Tyr Ile Asp Ile Val Asp Pro Phe
 225 230 235 240

Leu Thr Leu Lys Gly Leu Gln Leu Ile Tyr Glu Arg Asn Arg Val Gly
 245 250 255

Ser Val

<210> 10
 <211> 262
 <212> PRT
 <213> Deinocerurus radiopugnans

<400> 10
 Met Pro Ala Phe Pro Leu Leu Ala Val Asp Ile Gly Asn Thr Thr Thr
 1 5 10 15
 Val Leu Gly Leu Ala Asp Ala Ser Gly Ala Leu Thr His Thr Trp Arg
 20 25 30
 Ile Arg Thr Asn Arg Glu Met Leu Pro Asp Asp Leu Ala Leu Gln Leu
 35 40 45
 His Gly Leu Phe Thr Leu Ala Gly Ala Pro Ile Pro Arg Ala Ala Val
 50 55 60
 Leu Ser Ser Val Ala Pro Pro Val Gly Glu Asn Tyr Ala Leu Ala Leu
 65 70 75 80
 Lys Arg His Phe Met Ile Asp Ala Phe Ala Val Ser Ala Glu Asn Leu
 85 90 95
 Pro Asp Val Thr Val Glu Leu Asp Thr Pro Gly Ser Val Gly Ala Asp
 100 105 110
 Arg Leu Cys Asn Leu Phe Gly Ala Glu Lys Tyr Leu Gly Gly Leu Asp
 115 120 125
 Tyr Ala Val Val Val Asp Phe Gly Thr Ser Thr Asn Phe Asp Val Val
 130 135 140
 Gly Arg Gly Arg Arg Phe Leu Gly Gly Ile Leu Ala Thr Gly Ala Gln
 145 150 155 160
 Val Ser Ala Asp Ala Leu Phe Ala Arg Ala Lys Leu Pro Arg Ile
 165 170 175
 Thr Leu Gln Ala Pro Glu Thr Ala Ile Gly Lys Asn Thr Val His Ala
 180 185 190
 Leu Gln Ser Gly Leu Val Phe Gly Tyr Ala Glu Met Val Asp Gly Leu
 195 200 205
 Leu Arg Arg Ile Arg Ala Glu Leu Pro Gly Glu Ala Val Ala Val Ala
 210 215 220
 Thr Gly Gly Phe Ser Arg Thr Val Glu Gly Ile Cys Glu Glu Ile Asp
 225 230 235 240
 Tyr Tyr Asp Glu Thr Leu Thr Leu Arg Gly Leu Val Glu Leu Trp Ala
 245 250 255
 Ser Arg Ser Glu Val Arg
 260

<210> 11
 <211> 212
 <212> PRT
 <213> Desulfovibrio vulgaris

<400> 11
 Met Thr Gln His Phe Leu Leu Phe Asp Ile Gly Asn Thr Asn Val Lys
 1 5 10 15
 Ile Gly Ile Ala Val Glu Thr Ala Val Leu Thr Ser Tyr Val Leu Pro
 20 25 30
 Thr Asp Pro Gly Gln Thr Thr Asp Ser Ile Gly Leu Arg Leu Leu Glu
 35 40 45
 Val Leu Arg His Ala Gly Leu Gly Pro Ala Asp Val Gly Ala Cys Val
 50 55 60
 Ala Ser Ser Val Val Pro Gly Val Asn Pro Leu Ile Arg Arg Ala Cys
 65 70 75 80
 Glu Arg Tyr Leu Tyr Arg Lys Leu Leu Phe Ala Pro Gly Asp Ile Ala
 85 90 95
 Ile Pro Leu Asp Asn Arg Tyr Glu Arg Pro Ala Glu Val Gly Ala Asp
 100 105 110
 Arg Leu Val Ala Ala Tyr Ala Ala Arg Arg Leu Tyr Pro Gly Pro Arg
 115 120 125
 Ser Leu Val Ser Val Asp Phe Gly Thr Ala Thr Thr Phe Asp Cys Val
 130 135 140
 Glu Gly Gly Ala Tyr Leu Gly Gly Leu Ile Cys Pro Gly Val Leu Ser
 145 150 155 160
 Ser Ala Gly Ala Leu Ser Ser Arg Thr Ala Lys Leu Pro Arg Ile Ser
 165 170 175
 Leu Glu Val Glu Glu Asp Ser Pro Val Ile Gly Arg Ser Thr Thr Thr
 180 185 190
 Ser Leu Asn His Gly Phe Ile Phe Gly Phe Ala Ala Met Thr Glu Gly
 195 200 205
 Val Leu Ala Ala
 210

<210> 12
 <211> 246
 <212> PRT
 <213> Thermotoga maritima

<400> 11
 Met Tyr Leu Leu Val Asp Val Gly Asn Thr His Ser Val Phe Arg Ile
 1 5 10 15
 Thr Glu Asp Gly Lys Thr Ile Arg Arg Thr Asn Leu Ser Thr Gly Val
 20 25 30 35

Phe Gln Thr Val Asp Glu Leu Ile Ser His Leu His Pro Leu Leu Gly
 31 41 48
 Asp Ala Met Arg Glu Ile Lys Gly Ile Gly Val Ala Ser Val Val Pro
 50 58 61
 Thr Gln Asn Thr Val Ile Glu Arg Phe Ser Gln Lys Tyr Phe His Ile
 65 70 75 80
 Ser Pro Ile Trp Val Lys Ala Lys Asn Gly Cys Val Lys Trp Asn Val
 85 90 95
 Lys Asn Pro Ser Glu Val Gly Ala Asp Arg Val Ala Asn Val Val Ala
 100 105 110
 Phe Val Lys Glu Tyr Gly Lys Asn Gly Ile Ile Ile Asp Met Gly Thr
 115 120 125
 Ala Thr Thr Val Asp Leu Val Val Asn Gly Ser Tyr Glu Gly Gly Ala
 130 135 140
 Ile Leu Pro Gly Phe Phe Met Met Val His Ser Leu Phe Arg Gly Thr
 145 150 155 160
 Ala Lys Leu Pro Leu Val Glu Val Lys Pro Ala Asp Phe Val Val Gly
 165 170 175
 Lys Asp Thr Glu Glu Asn Ile Arg Leu Gly Val Val Asn Gly Ser Val
 180 185 190
 Tyr Ala Leu Glu Gly Ile Ile Gly Arg Ile Lys Glu Val Tyr Gly Asp
 195 200 205
 Leu Pro Val Val Leu Thr Gly Gly Gln Ser Lys Ile Val Lys Asp Met
 210 215 220
 Ile Lys His Glu Ile Phe Asp Glu Asp Leu Thr Ile Lys Gly Val Tyr
 225 230 235 240
 His Phe Cys Phe Gly Asp
 245

<210> 13
 <211> 273
 <212> PRT
 <213> *Treganema pallidum*

<400> 13
 Met Leu Leu Ile Asp Val Gly Asn Ser His Val Val Phe Gly Ile Gln
 1 5 10 15
 Gly Glu Asn Gly Gly Arg Val Lys Val Arg Glu Leu Phe Arg Leu Ala
 20 25 30 35
 Pro Asp Ala Arg Lys Thr Gln Asn Glu Tyr Ser Leu Leu Ile His Ala
 40 45 50 55
 Leu Tyr His Arg Ala Gly Val Gly Arg Ala Ser Leu Arg Asn Ala Ile
 60 65 70 75

Ile Ser Ser Val Val Phe Val Leu Thr Lys Thr Ile Ala Asp Ala Val
 80 70 90
 Ala Gln Ile Ser Gly Val Gln Pro Val Val Phe Gly Phe Trp Ala Tyr
 85 90 95
 Glu His Leu Pro Val Arg Ile Pro Glu Pro Val Arg Ala Glu Ile Gly
 100 105 110
 Thr Asp Leu Val Ala Asn Ala Val Ala Ala Tyr Val His Phe Arg Ser
 115 120 125
 Ala Cys Val Val Val Asp Cys Gly Thr Ala Leu Thr Phe Thr Ala Val
 130 135 140
 Asp Gly Thr Gly Leu Ile Gln Gly Val Ala Ile Ala Pro Gly Leu Arg
 145 150 155 160
 Thr Ala Val Gln Ser Leu His Thr Gly Thr Ala Gln Leu Pro Leu Val
 165 170 175
 Pro Leu Ala Leu Pro Asp Ser Val Leu Gly Lys Asp Thr Thr His Ala
 180 185 190
 Val Gln Ala Gly Val Val Arg Gly Thr Leu Phe Val Ile Arg Ala Met
 195 200 205
 Ile Ala Gln Cys Gln Lys Glu Leu Gly Cys Arg Cys Ala Ala Val Ile
 210 215 220
 Thr Gly Gly Leu Ser Arg Leu Phe Ser Ser Glu Val Asp Phe Pro Pro
 225 230 235 240
 Ile Asp Ala Gln Leu Thr Leu Ser Gly Leu Ala His Ile Ala Arg Leu
 245 250 255
 Val Pro Thr Ser Leu Leu Pro Pro Ala Thr Val Ser Gly Ser Ser Gly
 260 265 270

Asn

<210> 14
 <211> 262
 <212> PRT
 <213> Borrelia burgdorferi

<210> 14
 Met Asn Lys Pro Leu Leu Ser Glu Leu Ile Ile Asp Ile Gly Asp Thr
 1 5 10
 Ser Ile Ala Phe Ala Leu Phe Lys Asp Asn Phe Val Asn Leu Phe Ile
 21 25 29
 Lys Met Lys Thr Asn Leu Met Leu Arg Tyr Asp Ala Val Trp Ser Phe
 33 37 41
 Phe Glu His Asn Ile Asp Ile Asn Val Asn Lys Val Ile Ile Ser Ser
 45 49 53

Val Val Phe Ile Leu Asn Glu Thr Phe Lys Asn Val Ile Phe Ser Phe
65 75 80

Phe Lys Ile Lys Pro Leu Phe Ile Gly Phe Asp Leu Asn Tyr Asp Leu
85 90 95

Thr Phe Asn Pro Tyr Lys Ser Asp Lys Phe Leu Leu Gly Ser Asp Val
100 105 110

Phe Ala Asn Leu Val Ala Ala Ile Glu Asn Tyr Ser Phe Glu Asn Val
115 120 125

Leu Val Val Asp Leu Gly Thr Ala Cys Thr Ile Phe Ala Val Ser Arg
130 135 140

Gln Asp Gly Ile Leu Gly Gly Ile Ile Asn Ser Gly Pro Leu Ile Asn
145 150 155 160

Phe Asn Ser Leu Leu Asp Asn Ala Tyr Leu Ile Lys Lys Phe Pro Ile
165 170 175

Ser Thr Pro Asn Asn Leu Leu Glu Arg Thr Thr Ser Gly Ser Val Asn
180 185 190

Ser Gly Leu Phe Tyr Gln Tyr Lys Tyr Leu Ile Glu Gly Val Tyr Arg
195 200 205

Asp Ile Lys Gln Met Tyr Lys Lys Lys Phe Asn Leu Ile Ile Thr Gly
210 215 220

Gly Asn Ala Asp Leu Ile Leu Ser Leu Ile Glu Ile Glu Phe Ile Phe
225 230 235 240

Asn Ile His Leu Thr Val Glu Gly Val Arg Ile Leu Gly Asn Ser Ile
245 250 255

Asp Phe Lys Phe Val Asn
260

<210> 15
 <211> 229
 <212> PRT
 <213> Aquifex aeolicus

<400> 15
 Met Arg Phe Leu Thr Val Asp Val Gly Asn Ser Ser Val Asp Ile Ala
1 5 10

Leu Trp Glu Gly Lys Lys Val Lys Asp Phe Leu Lys Leu Ser His Gln
15 20 25 30

Glu Phe Leu Lys Glu Glu Phe Pro Lys Leu Lys Ala Leu Gly Ile Ser
35 40 45

Val Lys Ala Ser Phe Ser Glu Lys Val Arg Gly Lys Ile Pro Lys Ile
50 55 60

Lys Phe Leu Lys Lys Lys His Asn Phe Ile Ile His Val Asp Tyr Lys Thr
65 70 75 80

Pro Glu Thr Leu Gly Thr Asp Arg Val Ala Leu Ala Tyr Ser Ala Lys
 88 90 95
 Lys Phe Tyr Gly Lys Asn Val Val Val Ile Ser Ala Gly Thr Ala Leu
 100 105 110
 Val Ile Asp Leu Val Leu Glu Gly Lys Phe Lys Gly Gly Phe Ile Thr
 115 120 125
 Leu Gly Leu Gly Lys Lys Leu Lys Ile Leu Ser Asp Leu Ala Glu Gly
 130 135 140
 Ile Pro Glu Phe Phe Pro Glu Glu Val Glu Ile Phe Leu Gly Arg Ser
 145 150 155 160
 Thr Arg Glu Cys Val Leu Gly Gly Ala Tyr Arg Glu Ser Thr Glu Phe
 165 170 175
 Ile Lys Ser Thr Leu Lys Leu Trp Arg Lys Val Phe Lys Arg Lys Phe
 180 185 190
 Lys Val Val Ile Thr Gly Gly Glu Gly Lys Tyr Phe Ser Lys Phe Gly
 195 200 205
 Ile Tyr Asp Pro Leu Leu Val His Arg Gly Met Arg Asn Leu Leu Tyr
 210 215 220
 Leu Tyr His Arg Ile
 225

<210> 16
 <211> 257
 <212> PRT
 <213> Synechocystis sp.

<400> 16
 Met Glu Thr Ser Lys Pro Gly Cys Gly Leu Ala Leu Asp Asn Asp Lys
 1 5 10 15
 Gln Lys Pro Trp Leu Gly Leu Met Ile Gly Asn Ser Arg Leu His Trp
 20 25 30
 Ala Tyr Cys Ser Gly Asn Ala Pro Leu Gln Thr Trp Val Thr Asp Tyr
 35 40 45
 Asn Pro Lys Ser Ala Gln Leu Pro Val Leu Leu Gly Lys Val Pro Leu
 50 55 60
 Met Leu Ala Ser Val Val Pro Glu Gln Thr Glu Val Trp Arg Val Tyr
 65 70 75 80
 Gln Pro Lys Ile Leu Thr Leu Lys Asn Leu Pro Leu Val Asn Leu Tyr
 85 90 95
 Pro Ser Phe Gly Ile Asp Arg Ala Leu Ala Gly Leu Gly Thr Gly Leu
 100 105 110
 Thr Tyr Gly Phe Pro Lys Leu Val Val Asp Gly Gly Thr Ala Leu Thr
 115 120

Ile Thr Gly Phe Asp Gln Asp Lys Lys Leu Val Gly Gly Ala Ile Leu
 135 135 140
 Pro Gly Leu Gly Leu Gln Leu Ala Thr Leu Gly Asp Arg Leu Ala Ala
 145 150 155 160
 Leu Pro Lys Leu Glu Met Asp Gln Leu Thr Glu Leu Pro Asp Arg Trp
 165 170 175
 Ala Leu Asp Thr Pro Ser Ala Ile Phe Ser Gly Val Val Tyr Gly Val
 180 185 190
 Leu Gly Ala Leu Gln Ser Tyr Leu Gln Asp Trp Gln Lys Leu Phe Pro
 195 200 205
 Gly Ala Ala Met Val Ile Thr Gly Gly Asp Gly Lys Ile Leu His Gly
 210 215 220
 Phe Leu Lys Glu His Ser Pro Asn Leu Ser Val Ala Trp Asp Asp Asn
 225 230 235 240
 Leu Ile Phe Leu Gly Met Ala Ala Ile His His Gly Asp Arg Pro Ile
 245 250 255

Cys

<210> 17
 <211> 223
 <212> PRT
 <213> Helicobacter pylori

<400> 17
 Met Pro Ala Arg Gln Ser Phe Thr Asp Leu Lys Asn Leu Val Leu Cys
 1 5 10 15
 Asp Ile Gly Asn Thr Arg Ile His Phe Ala Gln Asn Tyr Gln Leu Phe
 20 25 30
 Ser Ser Ala Lys Glu Asp Leu Lys Arg Leu Gly Ile Gln Lys Glu Ile
 35 40 45
 Phe Tyr Ile Ser Val Asn Glu Glu Asn Glu Lys Ala Leu Leu Asn Cys
 50 55 60
 Tyr Pro Asn Ala Lys Asn Ile Ala Gly Phe Phe His Leu Gln Thr Asp
 65 70 75 80
 Tyr Val Gly Leu Gly Ile Asp Arg Gln Met Ala Cys Leu Ala Val Asn
 85 90 95
 Asn Gly Val Val Val Asp Ala Gly Ser Ala Ile Thr Ile Asp Leu Ile
 100 105 110
 Lys Glu Gly Lys His Leu Gly Gly Cys Ile Leu Pro Gly Leu Ala Glu
 115 120 125
 Tyr Ile His Ala Tyr Lys Lys Ser Ala Lys Ile Leu Gln Glu Pro Phe
 130 135 140

Lys Ala Leu Asp Ser Leu Glu Val Leu Pro Lys Ser Thr Arg Asp Ala
 145 155 160
 Val Asn Tyr Gly Met Val Leu Ser Val Ile Ala Cys Ile Glu His Leu
 165 170 175
 Ala Lys Asn Glu Lys Ile Tyr Leu Cys Gly Gly Asp Ala Lys Tyr Leu
 180 185 190
 Ser Ala Phe Leu Pro His Ser Val Cys Lys Glu Arg Leu Val Phe Asp
 195 200 205
 Gly Met Glu Ile Ala Leu Lys Lys Ala Gly Ile Leu Glu Cys Lys
 210 215 220

<210> 18
 <211> 267
 <212> PRT
 <213> Bordetella pertussis

<400> 18
 Met Ile Ile Leu Ile Asp Ser Gly Asn Ser Arg Leu Lys Val Gly Trp
 1 5 10 15
 Phe Asp Pro Asp Ala Pro Gln Ala Ala Arg Glu Pro Ala Pro Val Ala
 20 25 30
 Phe Asp Asn Leu Asp Leu Asp Ala Leu Gly Arg Trp Leu Ala Thr Leu
 35 40 45
 Pro Arg Arg Pro Gln Arg Ala Leu Gly Val Asn Val Ala Gly Leu Ala
 50 55 60
 Arg Gly Glu Ala Ile Ala Ala Thr Leu Arg Ala Gly Gly Cys Asp Ile
 65 70 75 80
 Arg Trp Leu Arg Ala Gln Pro Leu Ala Met Gly Leu Arg Asn Gly Tyr
 85 90 95
 Arg Asn Pro Asp Gln Leu Gly Ala Asp Arg Trp Ala Cys Met Val Gly
 100 105 110
 Val Leu Ala Arg Gln Pro Ser Val His Pro Pro Leu Leu Val Ala Ser
 115 120 125
 Phe Gly Thr Ala Thr Thr Leu Asp Thr Ile Gly Pro Asp Asn Val Phe
 130 135 140
 Pro Gly Gly Leu Ile Leu Pro Gly Pro Ala Met Met Arg Gly Ala Leu
 145 150 155 160
 Ala Tyr Gly Thr Ala His Leu Pro Leu Ala Asp Gly Leu Val Ala Asp
 165 170 175
 Tyr Pro Ile Asp Thr His Gln Ala Ile Ala Ser Gly Ile Ala Ala Ala
 180 185 190
 Glu Ala Gly Ala Ile Val Arg Gln Trp Leu Ala Gly Arg His Arg Tyr
 195 200 205

Gly Gln Ala Pro Glu Ile Tyr Val Ala Gly Gly Gly Trp Pro Glu Val
 210 215 220
 Arg Gln Glu Ala Glu Arg Leu Leu Ala Val Thr Gly Ala Ala Phe Gly
 225 230 235 240
 Ala Thr Pro Gln Pro Thr Tyr Leu Asp Ser Pro Val Leu Asp Gly Leu
 245 250 255
 Ala Ala Leu Ala Ala Gln Gly Ala Pro Thr Ala
 260 265

<210> 19
 <211> 777
 <212> DNA
 <213> Bacillus subtilis

<220>
 <221> CDS
 <222> (1)...(774)

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 Leu Leu Leu Val Ile Asp Val Gly Asn Thr Asn Thr Val Leu Gly Val
 1 5 10 15
 tat cat gat gga aaa tta gaa tat cac tgg cgt ata gaa aca agc agg 96
 Tyr His Asp Gly Lys Leu Glu Tyr His Trp Arg Ile Glu Thr Ser Arg
 20 25 30
 cat aaa aca gaa gat gag ttt ggg atg att ttg agt tcc tta ttt gat 144
 His Lys Thr Glu Asp Glu Phe Gly Met Ile Leu Arg Ser Leu Phe Asp
 35 40 45
 aac tcc ggg att atg ttt gaa cag ata gat ggc att att att tgg tca 192
 His Ser Gly Leu Met Phe Glu Gln Ile Asp Gly Ile Ile Ile Ser Ser
 50 55 60
 gta gtg cag cca atc atg ttt gaa tta gaa aga atg tcc aca aaa tac 240
 Val Val Pro Pro Ile Met Phe Ala Leu Glu Arg Met Cys Thr Lys Tyr
 65 70 75 80
 ttt cat atc gag cct caa att gtt ggt cca ggt atg aaa aat ggt tta 288
 Phe His Ile Glu Pro Gln Ile Val Gly Pro Gly Met Lys Thr Gly Leu
 85 90 95
 aat ata aaa tat gat aat cag aaa gaa ata ggg gaa tac aca atc gta 336
 Asn Ile Lys Tyr Asp Asn Pro Lys Glu Val Gly Ala Asp Arg Ile Val
 100 105 110
 aat ggt atc aat atg ata tac ttt tac ttt aat cca tta att att gtc 384
 Asn Ala Val Ala Ala Ile His Leu Tyr Gly Asn Pro Leu Ile Val Val
 115 120 125
 tat tta tta att att ata atg tat ttt tat att tat tta att ata aat 432
 Asp Phe Gly Thr Ala Thr Thr Tyr Cys Tyr Ile Asp Glu Asn Lys Gln
 130 135 140
 tat att att att att att att att att att att att att att att att 480
 Tyr Met Gly Gly Ala Ile Ala Leu Gly Ile Thr Ile Ser Thr Ala Ala

145	150	155	160	
ggt tac tgg ggt gaa gaa aag gtt gtt ggt atc gaa atc atc ggg gtc				848
Leu Tyr Ser Arg Ala Ala Lys Leu Pro Arg Ile Gln Ile Thr Arg Pro				
	168	170	175	
gac aat att atc gga aaa aac aat gtt agc gag atg caa tct gga att				876
Asp Asn Ile Ile Gly Lys Asn Thr Val Ser Ala Met Gln Ser Gly Ile				
	180	185	190	
cta ttt ggc tat gtc ggc caa gtg gaa gga atc gtt aag gga atg aaa				624
Leu Phe Gly Tyr Val Gly Gln Val Glu Gly Ile Val Lys Arg Met Lys				
	195	200	205	
tgg cag gaa aaa cag gac ctg aag gtc att gag aca gga ggc atg gag				672
Tyr Gln Ala Lys Gln Asp Leu Lys Val Ile Ala Thr Gly Gly Leu Ala				
	210	215	220	
cag ctg att gag aac gaa tca gat tgt ata gac atc gtt gat caa ttc				720
Pro Leu Ile Ala Asn Glu Ser Asp Cys Ile Asp Ile Val Asp Pro Phe				
	225	230	235	240
tta acc cta aaa ggg ctg gaa ttg att tat gaa aga aac cgc gta gga				768
Leu Thr Leu Lys Gly Leu Glu Leu Ile Tyr Glu Arg Asn Arg Val Gly				
	245	250	255	
agt gta tag				777
Ser Val				
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<213> Bacillus subtilis				
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<221> CDS				
<222> (1)...(957)				
<400> 20				
gtg aaa aat aaa gaa ctt aac cta cat act tta tat aca cag cac aat				48
Met Lys Asn Lys Glu Leu Asn Leu His Thr Leu Tyr Thr Gln His Asn				
	1	8	15	18
agg gag tct tgg tct ggt cct ggg ggg cat tgg tgg att ggt gta tct				96
Arg Gln Ser Trp Ser Gly Phe Gly Gly His Leu Ser Ile Ala Val Ser				
	21	28	35	38
gaa gaa gag gaa aaa gat atg gaa gaa tgg aat gat tat cta tct att				144
Glu Glu Glu Ala Lys Ala Val Glu Gly Leu Asn Asp Tyr Leu Ser Val				
	39	46	53	
aaa gaa atg gag aag atc tat att tta ctt gaa cgc tta ctt tat tta				180
Gln Glu Val Glu Thr Ile Tyr Ile Pro Leu Val Arg Leu Leu His Leu				
	54	61	68	
ggt ggt aag tct gaa ggt gaa ggt ggt ggt tat ggt gat gtt tct tgg				216
His Val Tyr Ser Ala Ala Glu Arg Asn Lys His Val Asn Val Phe Leu				
	72	79	86	
aat tat tta tat tta tta aat att tta tta att att tta tta tta tta				252
Asn Thr Thr Thr Thr Thr Asn Thr Thr Thr Thr Thr Thr Thr Thr Thr				
	87	94	101	

Lys	His	Pro	His	Ser	Ala	Lys	Ile	Pro	Phe	Ile	Ile	Gly	Ile	Ala	Gly	
				85					90					95		
agt	gtc	gga	gtc	gga	aaa	agc	agg	agg	ggg	agg	atc	ttg	cag	aaq	atg	336
Ser	Val	Ala	Val	Gly	Lys	Ser	Thr	Thr	Ala	Arg	Ile	Leu	Gln	Lys	Leu	
			100				105					110				
ctt	tgg	agt	ttg	ctt	gac	agt	cca	aaa	gtg	agg	ctt	atc	acg	aca	gat	384
Leu	Ser	Arg	Leu	Pro	Asp	Arg	Pro	Lys	Val	Ser	Leu	Ile	Thr	Thr	Asp	
		115				120					125					
ggc	ttt	tta	ttt	ctt	act	gac	gag	tig	aaa	aag	aaa	aat	atg	atg	tca	432
Gly	Phe	Leu	Phe	Pro	Thr	Ala	Glu	Leu	Lys	Lys	Lys	Asn	Met	Met	Ser	
	130					135				140						
aga	aaa	gga	ttt	ctt	gaa	agg	tat	gat	gta	aag	ggg	ctg	ctc	gaa	ttt	480
Arg	Lys	Gly	Phe	Pro	Glu	Ser	Tyr	Asp	Val	Lys	Ala	Leu	Leu	Glu	Phe	
145					150				155					160		
ttg	aat	gac	tta	aaa	tca	gga	aag	gac	agg	gta	aag	ggc	ccg	gtg	tat	528
Leu	Asn	Asp	Leu	Lys	Ser	Gly	Lys	Asp	Ser	Val	Lys	Ala	Pro	Val	Tyr	
			165				170							175		
tcc	cat	cta	acc	tat	gac	cgc	gag	gaa	ggc	gtg	ttc	gag	gtt	gta	gaa	576
Ser	His	Leu	Thr	Tyr	Asp	Arg	Glu	Glu	Gly	Val	Phe	Glu	Val	Val	Glu	
		180				185						190				
cag	ggg	gat	att	gtg	att	att	gaa	ggc	att	aat	gtt	ctt	cag	tgg	ccc	624
Gln	Ala	Asp	Ile	Val	Ile	Ile	Glu	Gly	Ile	Asn	Val	Leu	Gln	Ser	Pro	
		195				200						205				
acc	ttg	gag	gat	gac	cgg	gaa	aac	cgg	cgt	att	ttt	gtt	tcc	gat	ttc	672
Thr	Leu	Glu	Asp	Asp	Arg	Glu	Asn	Pro	Arg	Ile	Phe	Val	Ser	Asp	Phe	
	210				215					220						
tta	gat	ttt	tgg	att	tat	gtg	gat	ggg	gag	gaa	agg	agg	att	ttc	acc	720
Phe	Asp	Phe	Ser	Ile	Tyr	Val	Asp	Ala	Glu	Glu	Ser	Arg	Ile	Phe	Thr	
225					230				235					240		
agg	tat	tta	gag	cgt	ttt	cgc	ctg	ctt	cgg	gaa	aca	gct	ttt	caa	aat	768
Trp	Tyr	Leu	Glu	Arg	Phe	Arg	Leu	Leu	Arg	Glu	Thr	Ala	Phe	Gln	Asn	
		245				250						255				
ctt	gat	tca	tat	ttt	tat	aaa	ttt	aaa	gac	ttg	tcc	gat	cag	gag	ggt	816
Pro	Asp	Ser	Tyr	Phe	His	Lys	Phe	Lys	Asp	Leu	Ser	Asp	Gln	Glu	Ala	
		260				265						270				
gac	gag	atg	gca	gcc	tgg	att	tgg	gac	agt	gtc	aat	tgg	cgg	aat	tta	864
Asp	Glu	Met	Ala	Ala	Ser	Ile	Trp	Glu	Ser	Val	Asn	Arg	Pro	Asn	Leu	
	275					280					285					
tat	gaa	aat	att	ttg	cta	act	aaa	ttt	agg	tca	gat	ttc	aat	ttg	cgt	912
Tyr	Glu	Asn	Ile	Leu	Pro	Thr	Lys	Phe	Arg	Ser	Asp	Leu	Ile	Leu	Arg	
	290					295					300					
aat	tta	tac	gtt	tat	aat	tta	tta	tta	tta	tta	tta	tta	tta	tta	tta	960
Lys	Gly	Asp	Gly	His	Lys	Val	Glu	Glu	Val	Leu	Val	Arg	Arg	Val		
305					310					315						

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<212> DNA

<213> Bacillus subtilis

<220>

<221> CDS

<222> (1)...(873)

<400> 21

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ttg tag att ggt gta ttt gaa gaa gag gca aaa ggt gtg gaa gga tgg      43
Met Ser Ile Ala Val Ser Glu Glu Glu Ala Lys Ala Val Glu Gly Leu
      1              5              10              15

aat gat tat cta tct gtt gaa gaa gtg gag aag atc tat att cgg att      96
Asn Asp Tyr Leu Ser Val Glu Glu Val Glu Thr Ile Tyr Ile Pro Leu
      20              25              30

gtt cgc ttg att cat tta cat gtc aag tct gag gat gaa cgc aat aag      144
Val Arg Leu Leu His Leu His Val Lys Ser Ala Ala Glu Arg Asn Lys
      35              40              45

cat gtc aat gtt ttt ttg aag cac cca cat tca gcc aaa att cgg ttt      192
His Val Asn Val Phe Leu Lys His Pro His Ser Ala Lys Ile Pro Phe
      50              55              60

att atc ggc att gcc ggc agt gtc gca gtc gga aaa agc aag aag gag      240
Ile Ile Gly Ile Ala Gly Ser Val Ala Val Gly Lys Ser Thr Thr Ala
      65              70              75              80

cgg atc ttg gag aag ctg att tgg agt ttg cat gac cgt cca aaa gtg      288
Arg Ile Leu Gln Lys Leu Leu Ser Arg Leu Pro Asp Arg Pro Lys Val
      85              90              95

agc att atc aag ata gat ggt ttt tta ttt cat acg gtc gag gtg aaa      336
Ser Leu Ile Thr Thr Asp Gly Phe Leu Phe Pro Thr Ala Glu Leu Lys
      100              105              110

aag aaa aat atg atg tca aga aaa gga ttt cat gaa agc tat gat gta      384
Lys Lys Asn Met Met Ser Arg Lys Gly Phe Pro Glu Ser Tyr Asp Val
      115              120              125

aag gag ctg ctg gaa ttt ttg aat gac tta aaa tca gga aag gac agc      432
Lys Ala Leu Leu Glu Phe Leu Asn Asp Leu Lys Ser Gly Lys Asp Ser
      130              135              140

gta aag gcc cgg gtg tat tcc cat cta acc tat gac cgc gag gaa ggt      480
Val Lys Ala Pro Val Tyr Ser His Leu Thr Tyr Asp Arg Gln Gln Gly
      145              150              155              160

gtg ttc gag gtt gta gaa cag gag cat att gtg att att aaa ggc att      528
Val Phe Glu Val Val Glu Gln Ala Asp Ile Val Ile Ile Glu Gly Ile
      165              170              175

aat gtt att cag tgg aac aat ttt aat tat gat gac gac gaa aat tgg att      576
Asn Val Leu Gln Ser Pro Thr Leu Gln Asp Asp Arg His Asn Pro Arg
      180              185              190

ttt ttt att ttt att att ttt ttt ttt ttt att tat ttc att att att      624
Ile Ile Val Ser Asp Phe Phe Asp Phe Gln Ile Tyr Val Arg Ala His
      195              200

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gaa agc cgg att ttc act tgg tat tta gag cgt ttt cgc ctg ctt cgg 672
 Glu Ser Arg Ile Phe Thr Trp Tyr Leu Glu Arg Phe Arg Leu Leu Arg
 210 215 220
 gaa acc gct ttt caa aat cct gat tca tat ttt cat aaa ttt aaa gac 720
 Glu Thr Ala Phe Gln Asn Pro Asp Ser Tyr Phe His Lys Phe Lys Asp
 225 230 235 240
 ttg tcc gat cag gag gct gac gag atg gga gcc tgg att tgg gag agt 768
 Leu Ser Asp Gln Glu Ala Asp Glu Met Ala Ala Ser Ile Trp Glu Ser
 245 250 255
 gtc aac cgg cgg aat tta tat gaa aat att ttg cca act aaa ttc agg 816
 Val Asn Arg Pro Asn Leu Tyr Glu Asn Ile Leu Pro Thr Lys Phe Arg
 260 265 270
 tca gat ctc att ttg cgt aag gga gac ggg cat aag gtc gag gaa ttg 864
 Ser Asp Leu Ile Leu Arg Lys Gly Asp Gly His Lys Val Glu Glu Val
 275 280 285
 ttg gta agg agg gta tga 882
 Leu Val Arg Arg Val
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<210> 22
 <211> 846
 <212> DNA
 <213> *Bacillus subtilis*

<220>
 <221> CDS
 <222> (1)...(843)

<400> 22
 gtg gaa gga ttg aat gat tat cta ttt gtt gaa gaa ttg gag arg atc 48
 Met Glu Gly Leu Asn Asp Tyr Leu Ser Val Glu Glu Val Glu Thr Ile
 1 5 10 15
 tat att cgg ctt gtc cgc ttg att cat tta cat gtc aag tct acc gct 96
 Tyr Ile Pro Leu Val Arg Leu Leu His leu His Val Lys Ser Ala Ala
 21 25 31
 gaa cgc aat aag cat gtc aat gtt ttt ttg aag cac cca cat tca gcc 144
 Glu Arg Asn Lys His Val Asn Val Phe Leu Lys His Pro His Ser Ala
 36 42 48
 aaa att cgg ttt att aat ggc att gat ggt aat ttt gga ttc gga aaa 192
 Lys Ile Pro Phe Ile Ile Gly Ile Ala Gly Ser Val Ala Val Gly Lys
 54 58 60
 agc acc acc cgg cgg att ttg cag aag cta att ttg cgt ttt acc gac 240
 Ser Thr Thr Ala Arg Ile Leu Gln Lys Leu Leu Ser Arg Leu Pro Asp
 66 72 78
 ttt cca aaa gtt att att att acc acc tat att att tta att att att 288
 Arg Pro Lys Val Ser Leu Ile Thr Thr Asp Gly Ile Leu Ile Pro Thr
 84 90 96
 ttt tat tta acc aat aaa aat att att att tta gta acc tta tta tta 336
 Ala His Leu Lys Lys Lys Asn Met Met Ser Ala Lys Gly Ile Pro Glu
 102 108 114 120

1970-1971
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Pro Glu Gln Lys His Ser Phe Gln Met Asn Gln Thr Val Leu Asp Gly
 260 265 270

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 Leu Tyr Gly Gly Lys
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931

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 <213> Bacillus subtilis

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Gln Ala Gly Val Asp Met Ile Leu Val Gly Asp Ser Leu Gly Met Val
 35 40 45

Val Leu Gly Leu Asp Ser Thr Val Gly Val Thr Val Ala Asp Met Ile
 50 55 60

His His Thr Lys Ala Val Lys Arg Gly Ala Pro Asn Thr Phe Ile Val
 65 70 75 80

Thr Asp Met Pro Phe Met Ser Tyr His Leu Ser Lys Glu Asp Thr Leu
 85 90 95

Lys Asn Ala Ala Ala Ile Val Gln Gln Ser Gly Ala Asp Ala Leu Lys
 100 105 110

Leu Glu Gly Gly Glu Gly Val Phe Glu Ser Ile Arg Ala Leu Thr Leu
 115 120 125

Gly Gly Ile Pro Val Val Ser His Leu Gly Leu Thr Pro Gln Ser Val
 130 135 140

Gly Val Leu Gly Gly Tyr Lys Val Gln Gly Lys Asp Glu Gln Ser Ala
 145 150 155 160

Lys Lys Leu Ile Glu Asp Ser Ile Lys Cys Glu Glu Ala Gly Ala Met
 165 170 175

Met Leu Val Leu Glu Lys Val Pro Ala Glu Leu Thr Ala Lys Ile Ala
 180 185 190

Glu Thr Leu Ser Ile Pro Val Ile Gly Ile Gly Ala Gly Val Lys Ala
 195 200 205

Asp Gly Gln Val Leu Val Tyr His Asp Ile Ile Gly His Gly Val Gln
 210 215 220

Arg Thr Lys Lys Phe Val Lys Gln Tyr Thr Arg Ile Asp Gln Thr Ile
 225 230 235 240

Gln Thr Ala Ile Ser Gly Tyr Val Gln Asp Val Arg His Arg Ala Ile
 245 250 255 260

Pro Glu Gln Lys His Ser Phe Gln Met Asn Gln Thr Val Leu Asp Gly
 260 265 270

Leu Tyr Gly Gly Lys
 275

<210> 25

<211> 858

<212> DNA

<213> Bacillus subtilis

<220>

<221> CDS

<222> (1)..(858)

<400> 25

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 Met Arg Gln Ile Thr Asp Ile Ser Gln Leu Lys Glu Ala Ile Lys Gln
 1 5 10 15

tac cat tca gag gcc aag tca atc gga ttt gtt ccg acg atg ggg ttt 96
 Tyr His Ser Glu Gly Lys Ser Ile Gly Phe Val Pro Thr Met Gly Phe
 20 25 30

atg cat gag ggg cat tta acc tta gca gac aaa gca aga taa gaa aac 144
 Leu His Glu Gly His Leu Thr Leu Ala Asp Lys Ala Arg Gln Glu Asn
 35 40 45

gac gcc gtt att atg agt att ttt gtg aat cct gca caa ttc ggc cct 192
 Asp Ala Val Ile Met Ser Ile Phe Val Asn Pro Ala Gln Phe Gly Pro
 50 55 60

atg gaa gat ttt gaa gca tat atg ggc gat att gag cgg tat tta gat 240
 Asn Glu Asp Phe Glu Ala Tyr Pro Arg Asp Ile Glu Arg Asp Ala Ala
 65 70 75 80

gtt gaa gaa aac gcc gga gtc gat att ttt ttt acg cca gat gat cat 288
 Leu Ala Glu Asn Ala Gly Val Asp Ile Leu Phe Thr Pro Asp Ala His
 85 90 95

gat atg tat ccc ggt gaa aag aat gtc acg att cat gta gaa aga cgc 336
 Asp Met Tyr Pro Gly Glu Lys Asn Val Thr Ile His Val Glu Arg Arg
 100 105 110

aca aac gta tta tgc ggg cat tca aga gaa aaa cat ttt ttt ttt gtc 384
 Thr Asp Val Leu Cys Gly Arg Ser Arg Glu Gly His Phe Asp Gly Val
 115 120 125

gaa atc gta tta aag aag att tta aat ata gtc aag ccc att att gcc 432
 Ala Ile Val Leu Thr Lys Leu Phe Asn Leu Val Lys Pro Thr Arg Ala
 130 135 140

tat tta att tta aac gat att tta tta tta tta tta gtt ttt ttt tta 480
 Tyr Phe Gly Leu Lys Asp Ala Ala Ala Val Ala Val Val Asp Gly Leu
 145 150 155 160

tta tta gta tta tta atg att att tta tta tta att gtt ttt att att 528
 Ile Ser Asp Phe Phe Met Asp Ile Glu Leu Val Pro Val Arg Thr Val
 165 170 175 180

aga gag gaa gac ggc tta gcc aaa agc tct cgc aat gta tac tta aca 576
 Arg Glu Glu Asp Gly Leu Ala Lys Ser Ser Arg Asn Val Tyr Leu Thr
 187 188 190

ggt gag gaa aga aaa gaa ggc cct aag atg tat cgg gcc att caa aca 624
 Ala Glu Glu Arg Lys Glu Ala Pro Lys Leu Tyr Arg Ala Leu Glu Thr
 195 200 205

agt gag gaa att gtc caa gcc ggt gaa aga gat cct gaa gag gty ata 672
 Ser Ala Glu Leu Val Glu Ala Gly Glu Arg Asp Pro Glu Ala Val Ile
 210 215 220

aaa ggt gaa aaa gat atc att gaa aag act agc gga acc ata gac tat 720
 Lys Ala Ala Lys Asp Ile Ile Glu Thr Thr Ser Gly Thr Ile Asp Tyr
 225 230 235 240

gta gag att tat tcc tat cgg gaa ctc gag cct gty aat gaa att gct 768
 Val Glu Leu Tyr Ser Tyr Pro Glu Leu Glu Pro Val Asn Glu Ile Ala
 245 250 255

gga aag atg att atc gct gtt gca gtt gct ttt tca aaa gag cgt tta 816
 Gly Lys Met Ile Leu Ala Val Ala Val Ala Phe Ser Lys Ala Arg Leu
 260 265 270

ata gat aat atc att att gat att cga gaa atg gag aga ata 858
 Ile Asp Asn Ile Ile Ile Asp Ile Arg Glu Met Glu Arg Ile
 275 280 285

<210> 26

<211> 286

<212> 887

<213> *Bacillus subtilis*

<410> 16

Met Arg Glu Ile Thr Asp Ile Ser Glu Leu Lys Glu Ala Ile Lys Glu
 1 5 10 15

Tyr His Ser Glu Gly Lys Ser Ile Gly Phe Val Pro Thr Met Gly Phe
 20 25 30

Leu His Glu Gly His Leu Thr Leu Ala Asp Lys Ala Arg Glu Glu Asp
 35 40 45

Asp Ala Val Ile Met Ser Ile Phe Val Asn Pro Ala Glu Phe Gly Pro
 50 55 60

Asn Glu Asp Phe Glu Ala Tyr Pro Arg Asp Ile Glu Arg Asp Ala Ala
 65 70 75 80

Leu Ala Glu Asn Ala Gly Val Asp Ile Leu Phe Thr Pro Asp Ala His
 85 90 95

Asp Met Tyr Pro Gly Glu Lys Asn Val Thr Ile His Val His Arg Arg
 100 105 110

Thr Asp Val Leu Tyr Gly Arg Ser Arg Glu Gly His Phe Asp Gly Val
 115 120 125

Ala Ile Val Leu Thr Lys Leu Phe Asn Leu Val Lys Pro Thr Arg Ala

130 135 140
 Tyr Phe Gly Leu Lys Asp Ala Gln Gln Val Ala Val Val Asp Gly Leu
 145 150 155 161
 Ile Ser Asp Phe Phe Met Asp Ile Glu Leu Val Pro Val Asp Thr Val
 165 170 175
 Arg Glu Glu Asp Gly Leu Ala Lys Ser Ser Arg Asn Val Tyr Leu Thr
 181 185 190
 Ala Glu Glu Arg Lys Glu Ala Pro Lys Leu Tyr Arg Ala Leu Gln Thr
 195 200 205
 Ser Ala Glu Leu Val Gln Ala Gly Glu Arg Asp Pro Glu Ala Val Ile
 210 215 220
 Lys Ala Ala Lys Asp Ile Ile Glu Thr Thr Ser Gly Thr Ile Asp Tyr
 225 230 235 240
 Val Glu Leu Tyr Ser Tyr Pro Glu Leu Glu Pro Val Asn Glu Ile Ala
 245 250 255
 Gly Lys Met Ile Leu Ala Val Ala Val Ala Phe Ser Lys Ala Arg Leu
 260 265 270
 Ile Asp Asn Ile Ile Ile Asp Ile Arg Glu Met Glu Arg Ile
 275 280 285

<210> 27
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 <213> *Bacillus subtilis*

<220>
 <221> CDS
 <222> (1)...(381)

<400> 27
 atg tat cga aca atg atg agc ggc aaa att cac agg gaa aat att aag 48
 Met Tyr Arg Thr Met Met Ser Gly Lys Leu His Arg Ala Thr Val Thr
 1 5 11 15
 gaa gaa aac ctg aac tat gtg gga agc att aca att gat gaa gat gtc 96
 Glu Ala Asn Leu Asn Tyr Val Gly Ser Ile Thr Ile Asp Glu Asp Leu
 20 25 30
 att gat aat atg aga atg att aat aat gaa aaa ata gaa att gtg aat 144
 Ile Asp Ala Val Gly Met Leu Pro Asn Glu Lys Val Gln Ile Val Asn
 35 40 45
 aat aat aat gaa gaa ggt att gaa acg tac att att att att aat aat 192
 Asn Asn Asn Gly Ala Arg Glu Leu Glu Thr Tyr Ile Ile Phe Gly Lys Arg
 50 55 60
 aga att att att att att att att att att att att att att att att 240
 Gly Ser Gly Val Ile Tyr Leu Asn Gly Ala Ala Ala Arg Leu Val Gln
 65 70
 tta tta tta tta tta tta tta tta tta tta tta tta tta tta tta 288
 Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr

Glu Gly Asp Lys Val Ile Ile Ile Ser Tyr Lys Met Met Ser Asp Gln
 85 90 95

gaa gag gaa agc cat gag cag aaa ggg ggt gtt ctg aat gat caa aac 336
 Glu Ala Ala Ser His Glu Pro Lys Val Ala Val Leu Asn Asp Gln Asn
 100 105 110

aaa att gaa caa atg ctg ggg aac gaa caa ggc cgt aca att ttg 361
 Lys Ile Glu Gln Met Leu Gly Asn Glu Pro Ala Arg Thr Ile Leu
 115 120 125

<210> 28
 <211> 127
 <212> PRT
 <213> Bacillus subtilis

<400> 28
 Met Tyr Arg Thr Met Met Ser Gly Lys Leu His Arg Ala Thr Val Thr
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Glu Ala Asn Leu Asn Tyr Val Gly Ser Ile Thr Ile Asp Glu Asp Leu
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Ile Asp Ala Val Gly Met Leu Pro Asn Glu Lys Val Gln Ile Val Asn
 35 40 45

Asn Asn Asn Gly Ala Arg Leu Glu Thr Tyr Ile Ile Pro Gly Lys Arg
 50 55 60

Gly Ser Gly Val Ile Cys Leu Asn Gly Ala Ala Ala Arg Leu Val Gln
 65 70 75 80

Glu Gly Asp Lys Val Ile Ile Ile Ser Tyr Lys Met Met Ser Asp Gln
 85 90 95

Glu Ala Ala Ser His Glu Pro Lys Val Ala Val Leu Asn Asp Gln Asn
 100 105 110

Lys Ile Glu Gln Met Leu Gly Asn Glu Pro Ala Arg Thr Ile Leu
 115 120 125

<210> 28
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 <212> DNA
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 <222> (1)...(894)

<400> 28
 atg aaa att gaa att att ggt taa ttt ttt ggt att att att att att 48
 Met Lys Ile Gly Ile Ile Gly Gly Gly Ser Val Gly Leu Leu Lys Ala
 1 5 10 15

tat tat ttt tta att tat tat tat ttt ttt ttt att att att att att att 96
 Tyr Tyr Leu Ser Ser Tyr His Asp Val Thr Val Val Thr Arg Arg Gln
 20 25 30 35 40 45

gaa gag ggt gag gac att gag tct gaa gga atc egg ctt tat aaa ggc	144
Glu Gln Ala Ala Ile Gln Ser Glu Gly Ile Arg Leu Tyr Lys Gly	
35 40 45	
ggg gag gaa ttc agg ggt gat tgg agt gag gac aag agt atc aat tgg	192
Gly Glu Gln Phe Arg Ala Asp Cys Ser Ala Asp Thr Ser Ile Asn Ser	
50 55 60	
gac ttt gac ctg ctt gtc gtg aca gtg aag cag cat cag ctt caa tct	240
Asp Phe Asp Leu Leu Val Val Thr Val Lys Gln His Gln Leu Gln Ser	
65 70 75 80	
gtc ttt tgg tgg ctt gaa cga atc ggg aag acg aat ata tta ttt ttg	288
Val Phe Ser Ser Leu Glu Arg Ile Gly Lys Thr Asn Ile Leu Phe Leu	
85 90 95	
caa aac ggc atg ggg cat atc cac gac cta aaa gac tgg cac gtt ggc	336
Gln Asn Gly Met Gly His Ile His Asp Leu Lys Asp Trp His Val Gly	
100 105 110	
cat tcc att tat gtt gga atc gtt gag cac gga gct gta aga aaa tgg	384
His Ser Ile Tyr Val Gly Ile Val Glu His Gly Ala Val Arg Lys Ser	
115 120 125	
gat aca gct gtt gat cat aca ggc cta ggt gcg ata aaa tgg agc ggc	432
Asp Thr Ala Val Asp His Thr Gly Leu Gly Ala Ile Lys Trp Ser Ala	
130 135 140	
ttc gac gat gct gaa cca gac cgg ctg aac atc ttg ttt cag cat aac	480
Phe Asp Asp Ala Glu Pro Asp Arg Leu Asn Ile Leu Phe Gln His Asn	
145 150 155 160	
cat tgg gat att cgg att tat tat gag arg gat tgg tac agt cta ctg	528
His Ser Asp Phe Pro Ile Tyr Tyr Glu Thr Asp Trp Tyr Arg Leu Leu	
165 170 175	
aac ggc aag ctg att gta aat gag tgt att aat cat tta aat ggc tta	576
Thr Gly Lys Leu Ile Val Asn Ala Cys Ile Asn Pro Leu Thr Ala Leu	
180 185 190	
ttg caa gtg aaa aat gga gaa ctg ctg aca acg cca gct tat ctg gct	624
Leu Gln Val Lys Asn Gly Glu Leu Leu Thr Thr Pro Ala Tyr Leu Ala	
195 200 205	
ttt atg aag ctg gta ttt cag gag gga tgt cgc att tta aaa gtt gaa	672
Phe Met Lys Leu Val Phe Gln Glu Ala Cys Arg Ile Leu Lys Leu Glu	
210 215 220	
aat gaa aac aag gct tgg cag cag gtt caa gca gtt tgt ggg caa acg	720
Asn Glu Glu Lys Ala Trp Glu Arg Val Gln Ala Val Cys Gly Gln Thr	
225 230 235 240	
aaa gac aat gtt tca tca att ctg gtt cac gtc att gaa gtt cag caa	768
Lys Glu Asn Arg Ser Ser Met Leu Val Asp Val Ile Gly Gly Arg Glu	
245 250 255	
ttc taa ttt tct ttt att att gga tat tta tta aat taa tta aat ttt	816
Thr Glu Ala Asp Ala Ile Ile Gly Tyr Leu Leu Lys Glu Ala Ser Leu	
260 265 270	
taa gtt ttt tat ttt att att ctg tta cac ttt tta tat ttt att att aat	864

Gln Gly Leu Asp Ala Val His Leu Glu Phe Leu Tyr Gly Ser Ile Lys
 275 280 285

gga ttg gag gga aat aca aac aaa gtc ttt
 Ala Leu Glu Arg Asn Thr Asn Lys Val Phe
 290 295

894

<210> 30
 <211> 298
 <212> PRT
 <213> Bacillus subtilis

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 20 25 30

Glu Gln Ala Ala Ala Ile Gln Ser Glu Gly Ile Arg Leu Tyr Lys Gly
 35 40 45

Gly Glu Glu Phe Arg Ala Asp Cys Ser Ala Asp Thr Ser Ile Asn Ser
 50 55 60

Asp Phe Asp Leu Leu Val Val Thr Val Lys Gln His Gln Leu Gln Ser
 65 70 75 80

Val Phe Ser Ser Leu Glu Arg Ile Gly Lys Thr Asn Ile Leu Phe Leu
 85 90 95

Gln Asn Gly Met Gly His Ile His Asp Leu Lys Asp Trp His Val Gly
 100 105 110

His Ser Ile Tyr Val Gly Ile Val Glu His Gly Ala Val Arg Lys Ser
 115 120 125

Asp Thr Ala Val Asp His Thr Gly Leu Gly Ala Ile Lys Trp Ser Ala
 130 135 140

Phe Asp Asp Ala Glu Pro Asp Arg Leu Asn Ile Leu Phe Gln His Asn
 145 150 155 160

His Ser Asp Phe Pro Ile Tyr Tyr Glu Thr Asp Trp Tyr Arg Leu Leu
 165 170 175

Thr Gly Lys Leu Ile Val Asn Ala Cys Ile Asn Pro Leu Thr Ala Leu
 180 185 190

Leu Gln Val Lys Asn Gly Glu Leu Leu Thr Thr Pro Ala Tyr Leu Ala
 195 200 205

Phe Met Lys Leu Val Phe Gln Gln Ala Cys Arg Ile Leu Lys Leu Gln
 210 215 220

Asn His Gln Lys Ala Trp Gln Arg Val Gln Ala Val Cys Gly Gln Thr
 225 230 235 240

Lys Gln Asn Arg Ser Ser Met Leu Val Asp Val Ile Gly Gly Arg Gln
 245 250 255

Thr Glu Ala Asp Ala Ile Ile Gly Tyr Leu Leu Lys Gln Ala Ser Leu
260 265 270

Gln Gly Leu Asp Ala Val His Leu Gln Phe Leu Tyr Gly Ser Ile Lys
275 280 285

Ala Leu Glu Arg Asn Thr Asn Lys Val Phe
290 295

<210> 31
<211> 1725
<212> DNA
<213> Bacillus subtilis

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<222> (1)...(1722)

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aag atg agc gga gca tta atg ctg att gaa tca tta aaa aaa gag aaa 96
Thr Met Ser Gly Ala Leu Met Leu Ile Glu Ser Leu Lys Lys Glu Lys
20 25 30
gta gaa atg atc ttc ggt tat ccg gga ggg gat gag att aca att tac 144
Val Glu Met Ile Phe Gly Tyr Pro Gly Gly Ala Val Leu Pro Ile Tyr
35 40 45
gat aag ata ttc aat tca ggg tgg gta cat atc ttt ccc att aat aaa 142
Asp Lys Leu Tyr Asn Ser Gly Leu Val His Ile Leu Pro Arg His Glu
50 55 60
caa gga gca att cat gca ggc gag gga tac gca agg gcc tcc gga aaa 240
Gln Gly Ala Ile His Ala Ala Glu Gly Tyr Ala Arg Val Ser Gly Lys
65 70 75 80
cca ggt gta gtc att gcc aag tca ggg ccc gga gcc aca aac att gtt 288
Pro Gly Val Val Ile Ala Thr Ser Gly Pro Gly Ala Thr Asn Leu Val
85 90 95
aca ggc att gat gat gcc atg att cat tca tgg ccg tta ggc ttc ttt 336
Thr Gly Leu Ala Asp Ala Met Ile Asp Ser Leu Pro Leu Val Val Phe
100 105 110
aca ggg cag gta gca acc tct gta atc ggg agc gat gca ttt cad aaa 384
Thr Gly Gln Val Ala Thr Ser Val Ile Gly Ser Asp Ala Phe Val Glu
115 120 125
aca gat att tta ggg att aag att tta tta aca aca ttt aat ttt cad 432
Ala Asp Ile Leu Gly Ile Thr Met Pro Val Thr Lys His Ser Tyr Val
130 135 140
ttt ttt ttt ttt gaa gat ttt ttt ttt att ttt aca ttt ttt ttt ttt 480
Val Arg Val Pro Ala Asp Leu Pro Arg Ile Ile Lys Glu Ala Phe His
145 150 155 160 165

att gga aga att gga aga ccc gga cct gta ttg att gat att cag aaa Ile Ala Thr Thr Gly Arg Pro Gly Pro Val Leu Ile Asp Ile Pro Lys 165 170 175	828
gat gta gga aga att gaa gga gaa ttc agc tac gat cat gag atg aat Asp Val Ala Thr Ile Glu Gly Glu Phe Ser Tyr Asp His Glu Met Asn 180 185 190	876
ctc cag gga tac cag cag aca aca gag cag aat tat ttg cag atc cgc Leu Pro Gly Tyr Gln Pro Thr Glu Pro Asn Tyr Leu Gln Ile Arg 195 200 205	624
aag ctt gtg gaa ggc gtg agc agt ggc aaa aaa cag gtg atc ctg ggc Lys Leu Val Glu Ala Val Ser Ser Ala Lys Lys Pro Val Ile Leu Ala 210 215 220	672
ggt ggc ggc gta ctg cac gga aaa ggc tca gaa gaa tta aaa aat tat Gly Ala Gly Val Leu His Gly Lys Ala Ser Glu Glu Leu Lys Asn Tyr 225 230 235 240	720
gct gaa cag cag caa atc cct gtg gga cac acc ctt ttg ggc ctc gga Ala Glu Gln Gln Gln Ile Pro Val Ala His Thr Leu Leu Gly Leu Gly 245 250 255	768
ggc ttc cag gct gac cat cag ctt ttc cta ggc atg ggc gga atg cac Gly Phe Pro Ala Asp His Pro Leu Phe Leu Gly Met Ala Gly Met His 260 265 270	816
ggt aat tat aga gcc aat atg gcc ctt cat gaa tgt gat cta tta atc Gly Thr Tyr Thr Ala Asn Met Ala Leu His Glu Cys Asp Leu Leu Ile 275 280 285	864
agt atc gac gcc ggt ttt gat gac ctt gta aga gga aac ctg aaa cac Ser Ile Gly Ala Arg Phe Asp Asp Arg Val Thr Gly Asn Leu Lys His 290 295 300	912
ttt gcc aga aac gcc aag ata gcc cac atc gat att gat cca gct gaa Phe Ala Arg Asn Ala Lys Ile Ala His Ile Asp Ile Asp Pro Ala Glu 305 310 315 320	960
atr gga aaa atc atg aaa aca cac att cct gta gtc gga gac agc aaa Ile Gly Lys Ile Met Lys Thr Gln Ile Pro Val Val Gly Asp Ser Lys 325 330 335	1008
att gtc ctg cag gac ctg atc aaa caa gac ggc aaa caa agc cat tca Ile Val Leu Gln Gln Leu Ile Lys Gln Asp Gly Lys Gln Ser Asp Ser 340 345 350	1056
acc gaa tgg aaa aaa caa ctc gta gaa tgg aaa gaa gag tat cag ctc Ser Glu Trp Lys Lys Gln Leu Ala Gln Trp Lys Glu Glu Tyr Pro Leu 355 360 365	1104
tty tat gta cat aat gaa caa gaa ggt ttt aaa cct tcy aaa ttt att Trp Tyr Val Asp Asn Glu Gln Gln Gly Phe Lys Pro Gln Lys Leu Ile 370 375	1152
tta tat att att tta ttt aca aca tta tat att att att att att att Gln Tyr Ile His Gln Ile Thr Lys Gly Gln Ala Ile Val Ala Thr Asp 380 385	1200
tta ggt cag tat tta att ttt tta tta tta tta tta tta tta tta tta	1248

Val Gly Gln His Gln Met Trp Ser Ala Gln Phe Tyr Pro Phe Gln Lys
405 410 415

gca gat aaa tgg gtc acg tca ggc gga ttc gga acg atg gga ttc ggt 1296
Ala Asp Lys Trp Val Thr Ser Gly Gly Leu Gly Thr Met Gly Phe Gly
420 425 430

att ccg gcg gcg atc ggc gca cag ctg gcc gaa aaa gat got aac gtc 1344
Leu Pro Ala Ala Ile Gly Ala Gln Leu Ala Glu Lys Asp Ala Thr Val
435 440 445

gtc gcg gtt gtc gga gac ggc gga ttc caa atg acg att caa gaa ctc 1392
Val Ala Val Val Gly Asp Gly Gly Phe Gln Met Thr Leu Gln Glu Leu
450 455 460

gat gtt att ggc gaa tta aat ctt ccg gtc aag gta gtc att tta aat 1440
Asp Val Ile Arg Glu Leu Asn Leu Pro Val Lys Val Val Ile Leu Asn
465 470 475 480

aac got tgt ctc gga atg gtc aga cag tgg cag gaa att ttc tat gaa 1488
Asn Ala Cys Leu Gly Met Val Arg Gln Trp Gln Glu Ile Phe Tyr Glu
485 490 495

gaa cgt tat tca gaa tct aaa ttc got tct cag cct gac ttc gtc aaa 1536
Glu Arg Tyr Ser Glu Ser Lys Phe Ala Ser Gln Pro Asp Phe Val Lys
500 505 510

ttg tcc gaa gca tac ggc att aaa ggc atc aga att tca tca gaa ggc 1584
Leu Ser Glu Ala Tyr Gly Ile Lys Gly Ile Arg Ile Ser Ser Glu Ala
515 520 525

gaa gca aag caa aag ctg gaa gag gaa tta aca tca aga gaa cct gtc 1632
Glu Ala Lys Gln Lys Leu Gln Gln Ala Leu Thr Ser Arg Glu Pro Val
530 535 540

gtc att gac ggc cgg ggt gcc agt gaa gaa aaa gta ttc cag atg gtc 1680
Val Ile Asp Val Arg Val Ala Ser Glu Glu Lys Val Phe Pro Met Val
545 550 555 560

gct ccg ggc aaa ggc ctg cat gaa atg gtc ggc gtc aaa cct tga 1728
Ala Pro Gly Lys Gly Leu His Glu Met Val Gly Val Lys Pro
565 570

<210> 32

<211> 574

<212> PRT

<213> *Bacillus subtilis*

<400> 32

Met Gly Thr Asn Val Gln Val Asp Ser Ala Ser Ala Gln Lys Thr Gln
1 5 10 15Thr Met Ser Gly Ala Leu Met Leu Ile Glu Ser Leu Lys Lys Glu Lys
20 25 30 35 40Val Glu Met Ile Thr Gly Tyr Pro Gly Gly Ala Val Leu Pro Ile Tyr
45 50 55 60Asp Lys Leu Tyr Asn Ser Gly Leu Val His Ile Leu Pro Arg His His
65 70 75 80 85 90

Gln Gly Ala Ile His Ala Ala Glu Gly Tyr Ala Arg Val Ser Gly Lys
 65 70 75 80
 Pro Gly Val Val Ile Ala Thr Ser Gly Pro Gly Ala Thr Asn Leu Val
 85 90 95
 Thr Gly Leu Ala Asp Ala Met Ile Asp Ser Leu Pro Leu Val Val Phe
 100 105 110
 Thr Gly Gln Val Ala Thr Ser Val Ile Gly Ser Asp Ala Phe Gln Glu
 115 120 125
 Ala Asp Ile Leu Gly Ile Thr Met Pro Val Thr Lys His Ser Tyr Gln
 130 135 140
 Val Arg Gln Pro Glu Asp Leu Pro Arg Ile Ile Lys Glu Ala Phe His
 145 150 155 160
 Ile Ala Thr Thr Gly Arg Pro Gly Pro Val Leu Ile Asp Ile Pro Lys
 165 170 175
 Asp Val Ala Thr Ile Glu Gly Glu Phe Ser Tyr Asp His Glu Met Asn
 180 185 190
 Leu Pro Gly Tyr Gln Pro Thr Thr Glu Pro Asn Tyr Leu Gln Ile Arg
 195 200 205
 Lys Leu Val Glu Ala Val Ser Ser Ala Lys Lys Pro Val Ile Leu Ala
 210 215 220
 Gly Ala Gly Val Leu His Gly Lys Ala Ser Glu Glu Leu Lys Asn Tyr
 225 230 235 240
 Ala Glu Gln Gln Gln Ile Pro Val Ala His Thr Leu Leu Gly Leu Gly
 245 250 255
 Gly Phe Pro Ala Asp His Pro Leu Phe Leu Gly Met Ala Gly Met His
 260 265 270
 Gly Thr Tyr Thr Ala Asn Met Ala Leu His Glu Cys Asp Leu Leu Ile
 275 280 285
 Ser Ile Gly Ala Arg Phe Asp Asp Arg Val Thr Gly Asn Leu Lys His
 290 295 300
 Phe Ala Arg Asn Ala Lys Ile Ala His Ile Asn Ile Asp Pro Ala Glu
 305 310 315 320
 Ile Gly Lys Ile Met Lys Thr Gln Ile Pro Val Val Gly Asp Ser Lys
 325 330 335
 Ile Val Leu Gln Glu Leu Ile Lys Gln Asp Gly Lys Gln Ser Asp Ser
 340 345 350
 Ser Gln Thr Lys Lys Gln Leu Ala Gln Thr Lys Gln Gln Tyr Pro Leu
 355 360 365
 Asp Tyr Val Asp Asn Gln His Gln Gly His Lys Arg Gln Lys Leu Ile
 370 375 380

His Tyr Ile His Gln Phe Thr Lys Gly Glu Ala Ile Val Ala Thr Asp
385 390 395 400

Val Gly Gln His Gln Met Trp Ser Ala Gln Phe Tyr Pro Phe Gln Lys
405 410 415

Ala Asp Lys Trp Val Thr Ser Gly Gly Leu Gly Thr Met Gly Phe Gly
420 425 430

Leu Pro Ala Ala Ile Gly Ala Gln Leu Ala Gln Lys Asp Ala Thr Val
435 440 445

Val Ala Val Val Gly Asp Gly Gly Phe Gln Met Thr Leu Gln Glu Leu
450 455 460

Asp Val Ile Arg Glu Leu Asn Leu Pro Val Lys Val Val Ile Leu Asn
465 470 475 480

Asn Ala Cys Leu Gly Met Val Arg Gln Trp Gln Glu Ile Phe Tyr Glu
485 490 495

Glu Arg Tyr Ser Glu Ser Lys Phe Ala Ser Gln Pro Asp Phe Val Lys
500 505 510

Leu Ser Glu Ala Tyr Gly Ile Lys Gly Ile Arg Ile Ser Ser Glu Ala
515 520 525

Glu Ala Lys Glu Lys Leu Glu Glu Ala Leu Thr Ser Arg Glu Pro Val
530 535 540

Val Ile Asp Val Arg Val Ala Ser Glu Glu Lys Val Phe Pro Met Val
545 550 555 560

Ala Pro Gly Lys Gly Leu His Gln Met Val Gly Val Lys Pro
565 570

<210> 33

<211> 525

<212> DNA

<213> Bacillus subtilis

<220>

<221> CDS

<222> (1)...(522)

<410> 33

ttt aaa aga att atc aca tta act gta gta aat cat ttt ttt ttt tta 47
Met Lys Arg Ile Ile Thr Leu Thr Val Val Asn Arg Ser Gly Val Leu
1 5 10 15

aac cgt atc aac ggt cta tta aca aat agt cat taa aac att aaa agc 50
Asn Arg Ile Thr Gly Leu Phe Thr Lys Arg His Tyr Asn Ile Glu Ser
20 25 30

att tta ttt ttt tat aca tta aca ttt ttt ttt ttt ttt ttt ttt 144
Ile Thr Val Gly His Thr Gln Thr Ala Gly Val Ser Arg Ile Thr Phe
35 40 45

tta ttt tat ttt tta ttt tta aat ttt ttt tta tat tta aat aat 147
Val Val His Val His Gly His Asn Asp Val Gln Gln Leu Thr Lys His
50 55 60

51	55	60	
ctc aac aaa bag att gat gtg ctg aaa gtc aca gac atc aca aat caa	240		
Leu Asn Lys Gln Ile Asp Val Leu Lys Val Thr Asp Ile Thr Asn Gln			
65 70 75 80			
tgg att gtc bag agg gag ctg gcc tta atc aag gtt gtc tcc gca cct	288		
Ser Ile Val Gln Arg Glu Leu Ala Leu Ile Lys Val Val Ser Ala Pro			
85 90 95			
tca aca aga aca gag att aat gga atc ata gaa ccg ttt aga gcc tat	336		
Ser Thr Arg Thr Glu Ile Asn Gly Ile Ile Glu Pro Phe Arg Ala Ser			
100 105 110			
gtc gtt gat gtc agc aga gac agc atc gtt gtt cag gtg aca ggt gaa	384		
Val Val Asp Val Ser Arg Asp Ser Ile Val Val Gln Val Thr Gly Glu			
115 120 125			
tct aac aaa att gaa gcg ctt att gag tta tta aaa cct tat gcc att	432		
Ser Asn Lys Ile Glu Ala Leu Ile Glu Leu Leu Lys Pro Tyr Gly Ile			
130 135 140			
aaa gaa atc gcg aga aca ggt aca agc gct ttt gcg agg gga acc agc	480		
Lys Glu Ile Ala Arg Thr Gly Thr Thr Ala Phe Ala Arg Gly Thr Ser			
145 150 155 160			
aaa agg cgt cat cca ata aaa caa tat cta tgg tat aaa aca taa	528		
Lys Arg Arg His Pro Ile Lys Gln Tyr Leu Leu Tyr Lys Thr			
165 170			

<210> 34

<211> 174

<212> PRT

<213> Bacillus subtilis

<400> 34

Met Lys Arg Ile Ile Thr Leu Thr Val Val Asn Arg Ser Gly Val Leu	1 5 10 15
Asn Arg Ile Thr Gly Leu Phe Thr Lys Arg His Tyr Asn Ile Glu Ser	20 25 30
Ile Thr Val Gly His Thr Glu Thr Ala Gly Val Ser Arg Ile Thr Phe	35 40 45
Val Val His Val Glu Gly Glu Asn Asp Val Glu Glu Leu Thr Lys Glu	50 55 60
Leu Asn Lys Gln Ile Asp Val Leu Lys Val Thr Asp Ile Thr Asn Glu	65 70 75 80
Ser Ile Val Gln Arg Glu Leu Ala Leu Ile Lys Val Val Ser Ala Pro	85 90 95
Ser Thr Arg Thr Glu Ile Asn Gly Ile Ile Glu Ile Thr Arg Ala Ser	100 105 110 115
Val Val Asp Val Ser Arg Asp Ser Ile Val Val His Val Thr Gly Glu	120 125

Ser Asn Lys Ile Glu Ala Leu Ile Glu Leu Leu Lys Pro Tyr Gly Ile
130 135 140

Lys Glu Ile Ala Arg Thr Gly Thr Thr Ala Phe Ala Arg Gly Thr Ser
145 150 155 160

Lys Arg Arg His Pro Ile Lys Gln Tyr Leu Leu Tyr Lys Thr
165 170

<210> 35

<211> 1029

<212> DNA

<213> *Bacillus subtilis*

<220>

<221> CDS

<222> (1)...(1026)

<400> 35

atg gta aaa gta tat tat aac ggt gat atc aaa gag aac gla ttg got 48
Met Val Lys Val Tyr Tyr Asn Gly Asp ile Lys Glu Asn Val Leu Ala
1 5 10 15

gga aaa aca gta gag gtt atc ggg tac ggt tgg caa ggc cac gca cat 96
Gly Lys Thr Val Ala Val ile Gly Tyr Gly Ser Gln Gly His Ala His
20 25 30

ggt atg aac att aaa gaa agc gga gta gac gtg atc gtc ggt gtt aga 144
Ala Leu Asn Leu Lys Glu Ser Gly Val Asp Val ile Val Gly Val Arg
35 40 45

caa gga aaa att ttc aat caa gac caa gaa gac gga cat aaa gla ttt 192
Gln Gly Lys Ser Phe Thr Gln Ala Gln Glu Asp Gly His Lys Val Phe
50 55 60

tca gta aaa gaa atg gaa gac caa gac gaa atc atc atg gtt atg att 240
Ser Val Lys Glu Ala Ala Ala Gln Ala Glu ile ile Met Val Leu Leu
65 70 75 80

ccg gat gag cag cag caa aaa gta tac gaa got gaa atc aaa gat gaa 288
Pro Asp Glu Gln Gln Gln Lys Val Tyr Glu Ala Glu ile Lys Asp Glu
85 90 95

ttg aca gca gga aaa tca tta gta ttc got cat gga ttt aac atg cat 336
Leu Thr Ala Gly Lys Ser Leu Val Phe Ala His Gly Phe Asn Val His
100 105 110

ttc cat caa att att cat ccg ccg gat gta gat gta ttc tta gty gac 384
Phe His Gln ile Val Pro Pro Ala Asp Val Asp Val Phe Leu Val Ala
115 120 125

cat aaa att att gga cat ttg gta aca aga aca cat gag caa gaa gtt 432
Pro Lys Gly Pro Gly His Leu Val Arg Arg Thr Tyr Gln Gln Gly Ala
130 135 140

gac tta att tta att att att att att att att att att att att att 480
Gly Val Lys Ala Leu Phe Ala ile Tyr Gln Asp Val Thr Gly Gln Ala
145 150 155 160

att att att att att att att att att att att att att att att att 528

Arg Asp Lys Ala Leu Ala Tyr Ala Lys Gly Ile Gly Gly Ala Arg Ala
 165 170 175
 ggc gta tta gaa acg aca ttt aaa gaa gaa aca gaa aca gat ttg ttc 576
 Gly Val Leu Glu Thr Thr Phe Lys Glu Glu Thr Glu Thr Asp Leu Phe
 180 185 191
 ggt gag caa gca gtt ctt tgc ggc gga tta agc ggc ctt gtc aaa gcc 624
 Gly Glu Gln Ala Val Leu Cys Gly Gly Leu Ser Ala Leu Val Lys Ala
 195 200 205
 gga ttt gaa acc tta act gaa gca ggt tat cag cct gaa ctt gca tac 672
 Gly Phe Glu Thr Leu Thr Glu Ala Gly Tyr Gln Pro Glu Leu Ala Tyr
 210 215 220
 ttc gag tgt ctt cat gag ctg aaa tta atc gta gac ctt atg tac gaa 720
 Phe Glu Cys Leu His Glu Leu Lys Leu Ile Val Asp Leu Met Tyr Glu
 225 230 235 240
 gaa gga ctt gca gga atg aga tat tca atc tct gac aca gca cag tgg 768
 Glu Gly Leu Ala Gly Met Arg Tyr Ser Ile Ser Asp Thr Ala Gln Trp
 245 250 255
 gga gat ttc gta tca ggc cct cgc gtt gtg gac gcc aaa gta aaa gaa 816
 Gly Asp Phe Val Ser Gly Pro Arg Val Val Asp Ala Lys Val Lys Glu
 260 265 270
 tat atg aaa gaa gta tta aaa gat atc caa aac ggt aca ttc gca aaa 864
 Ser Met Lys Glu Val Leu Lys Asp Ile Gln Asn Gly Thr Phe Ala Lys
 275 280 285
 gag tgg atc gtc gaa aac caa gta aac cgt cct cgt ttc aac gct atc 912
 Glu Trp Ile Val Glu Asn Gln Val Asn Arg Pro Arg Phe Asn Ala Ile
 290 295 300
 aat caa agt gag aac gaa cat caa atc gaa gta gtg aga aga aag ctt 960
 Asn Ala Ser Glu Asn Glu His Gln Ile Glu Val Val Gly Arg Lys Leu
 305 310 315 320
 cgt gaa atg atg cgc ttt gtg aaa caa ggc aag aag aag gaa ggc gtg 1008
 Arg Glu Met Met Pro Phe Val Lys Gln Gly Lys Lys Lys Glu Ala Val
 325 330 335
 gtc tcc gtt ggc caa aat taa 1028
 Val Ser Val Ala Gln Asn
 340

<210> 36

<211> 342

<212> BRT

<213> Bacillus subtilis

<400> 36

Met Val Lys Val Tyr Tyr Asn Gly Asp Ile Lys Glu Asn Val Leu Ala
 1 1 1

Gly Lys Thr Val Ala Val Ile Gly Tyr Gly Ser Glu Gly His Ala His
 1 1

Ala Leu Asn Leu Lys Glu Ser Gly Val Asp Val Ile Val Gly Val Arg

35	40	45
Gln Gly Lys Ser Phe Thr	Gln Ala Gln Glu Asp	Gly His Lys Val Phe
50	55	60
Ser Val Lys Glu Ala Ala	Ala Gln Ala Glu Ile Ile	Met Val Leu Leu
65	70	75
Pro Asp Glu Gln Gln Gln	Lys Val Tyr Glu Ala Glu	Ile Lys Asp Glu
85	90	95
Leu Thr Ala Gly Lys Ser	Leu Val Phe Ala His	Gly Phe Asn Val His
100	105	110
Phe His Gln Ile Val Pro	Pro Ala Asp Val Asp	Val Phe Leu Val Ala
115	120	125
Pro Lys Gly Pro Gly His	Leu Val Arg Arg Thr	Tyr Glu Gln Gly Ala
130	135	140
Gly Val Pro Ala Leu Phe	Ala Ile Tyr Gln Asp	Val Thr Gly Glu Ala
145	150	155
Arg Asp Lys Ala Leu Ala	Tyr Ala Lys Gly Ile	Gly Gly Ala Arg Ala
165	170	175
Gly Val Leu Glu Thr Thr	Phe Lys Glu Glu Thr	Glu Thr Asp Leu Phe
180	185	190
Gly Glu Gln Ala Val Leu	Cys Gly Glu Leu Ser	Ala Leu Val Lys Ala
195	200	205
Gly Phe Glu Thr Leu Thr	Glu Ala Gly Tyr Gln	Pro Glu Leu Ala Tyr
210	215	220
Phe Gln Cys Leu His Glu	Leu Lys Leu Ile Val	Asp Leu Met Tyr Glu
225	230	235
Glu Gly Leu Ala Gly Met	Arg Tyr Ser Ile Ser	Asp Thr Ala Gln Trp
245	250	255
Gly Asp Phe Val Ser Gly	Pro Arg Val Val Asp	Ala Lys Val Lys Glu
260	265	270
Ser Met Lys Glu Val Leu	Lys Asp Ile Gln Asn	Gly Thr Phe Ala Lys
275	280	285
Glu Trp Ile Val Glu Asn	Gln Val Asn Arg Pro	Arg Phe Asn Ala Ile
290	295	300
Asn Ala Ser Glu Asn Glu	His Gln Ile Glu Val	Val Gly Arg Lys Leu
305	310	315
Arg Glu Met Met Pro Phe	Val Lys Gln Gly Lys	Lys Lys Glu Ala Val
320	325	330
Val Ser Val Ala Gln Asn		
335		

<211> 1674

<212> DNA

<213> *Bacillus subtilis*

<220>

<221> CDS

<222> (1)...(1674)

<400> 37

atg gca gaa tta cgc agt aat atg atc aca caa gga atc gat aga got	48
Met Ala Glu Leu Arg Ser Asn Met Ile Thr Gln Gly Ile Asp Arg Ala	
1 5 10 15	

cag cac cgc agt ttg ctt cgt gca gca ggg gta aaa gaa gag gat ttc	96
Pro His Arg Ser Leu Leu Arg Ala Ala Gly Val Lys Glu Glu Asp Phe	
20 25 30	

ggc aag cag ttt att gcg gtc tgt aat tca taa att gat atc gtt ccc	144
Gly Lys Pro Phe Ile Ala Val Cys Asn Ser Tyr Ile Asp Ile Val Pro	
35 40 45	

ggc cat gtt cac ttg cag gag ttt ggg aaa atc gta aaa gaa gca atc	192
Gly His Val His Leu Gln Glu Phe Gly Lys Ile Val Lys Glu Ala Ile	
50 55 60	

aga gaa gca ggg ggc gtt ccg ttc gaa ttc aat acc att ggg gta gat	240
Arg Glu Ala Gly Gly Val Pro Phe Glu Phe Asn Thr Ile Gly Val Asp	
65 70 75 80	

gat ggc atc gca atg ggg cat atc ggt atg aga tat ccg ctg cca agc	288
Asp Gly Ile Ala Met Gly His Ile Gly Met Arg Tyr Ser Leu Pro Ser	
85 90 95	

cgt gaa att atc gca gac tct gtc gaa aac gtt tta tca gca cac tgg	336
Arg Glu Ile Ile Ala Asp Ser Val Glu Thr Val Val Ser Ala His Trp	
100 105 110	

ttc gac gga atg gtc tgt att ccg aac tgc gac aaa atc aca ccg gga	384
Phe Asp Gly Met Val Cys Ile Pro Asn Cys Asp Lys Ile Thr Pro Gly	
115 120 125	

atg ctt atg gcg gca atg cgc atc aac att ccg aac att ttt gtc agc	432
Met Leu Met Ala Ala Met Arg Ile Asn Ile Pro Thr Ile Phe Val Ser	
130 135 140	

ggc gga ccg atg gcg gca gga aga aca agt taa ggc gga aaa atc taa	480
Gly Gly Pro Met Ala Ala Gly Arg Thr Ser Tyr Gly Arg Lys Ile Ser	
145 150 155 160	

ctt tcc tca gta ttc gaa ggc gta gtc gtc taa caa gca ggc aaa atc	528
Leu Ser Ser Val Phe Glu Gly Val Gly Ala Tyr Gln Ala Gly Lys Ile	
165 170 175	

aac gaa aac gac att caa gaa gta gac gac ttc gaa taa gaa aac ttc	576
Asn Glu Asn Glu Leu Gln Glu Leu Gln Gln Glu Gly Tyr Pro Thr Cys	
180 185 190	

ggt ttt ttt tca ggt att ttt aat ggt aac taa gta gta att ttt ttt	624
Gly Ser Lys Ser Gly Met Phe Thr Ala Asn Ser Met Asn Tyr Leu Ser	
195 200 205	

Leu Ala Pro Thr Ser Gln Ile Val Gly Met Gly Leu Gly Pro Lys Val
450 455 460

gga ttg att aag gac gga cgt ttt tcc gga ggc tcc cgt ggc ctc tca 1440
Ala Leu Ile Thr Asp Gly Arg Phe Ser Gly Ala Ser Arg Gly Leu Ser
465 470 475 480

atc ggc cac gta tca cct gag ggc gct gag ggc ggg ccg ctt ggc ttt 1488
Ile Gly His Val Ser Pro Gln Ala Ala Gln Gly Gly Pro Leu Ala Phe
485 490 495

gtt gaa aac gga gac cat att atc gtt gat att gaa aaa cgc atc ttg 1536
Val Gln Asn Gly Asp His Ile Ile Val Asp Ile Gln Lys Arg Ile Leu
500 505 510

gat gta aaa gtg cta gaa gaa gag tgg gaa aaa cga aaa ggc aac tgg 1584
Asp Val Gln Val Pro Gln Gln Gln Trp Gln Lys Arg Lys Ala Asn Trp
515 520 525

aaa ggt ttt gaa ccg aaa gtg aaa acc ggc tac ctg gca cgt tat tct 1632
Lys Gly Phe Gln Pro Lys Val Lys Thr Gly Tyr Leu Ala Arg Tyr Ser
530 535 540

aaa ctt gtg aca agt gcc aac acc ggc ggt att atg aaa atc 1674
Lys Leu Val Thr Ser Ala Asn Thr Gly Gly Ile Met Lys Ile
545 550 555

<210> 38

<211> 558

<212> BGI

<213> Bacillus subtilis

<400> 38

Met Ala Gln Leu Arg Ser Asn Met Ile Thr Gln Gly Ile Asp Arg Ala
1 10 15

Pro His Arg Ser Leu Leu Arg Ala Ala Gly Val Lys Gln Gln Asp Phe
20 25 30

Gly Lys Pro Phe Ile Ala Val Cys Asn Ser Tyr Ile Asp Ile Val Pro
35 40 45

Gly His Val His Leu Gln Gln Phe Gly Lys Ile Val Lys Gln Ala Ile
50 55 60

Arg Gln Ala Gly Gly Val Pro Phe Gln Phe Asn Thr Ile Gly Val Asp
65 70 75 80

Asp Gly Ile Ala Met Gly His Ile Gly Met Arg Tyr Ser Leu Pro Ser
85 90 95

Arg Gln Ile Ile Ala Asp Ser Val Gln Thr Val Val Ser Ala His Trp
100 105 110

Phe Asp Gly Met Val Lys Ile Ile Asn Lys Asp Lys Ile Thr Phe Gly
115 120 125

Met Leu Met Ala Ala Met Arg Ile Asn Ile Ile Thr Ile Phe Val Ser
130 135 140

Gly Gly Pro Met Ala Ala Gly Arg Thr Ser Tyr Gly Arg Lys Ile Ser
 148 150 155 160
 Leu Ser Ser Val Phe Glu Gly Val Gly Ala Tyr Gln Ala Gly Lys Ile
 165 170 175
 Asn Glu Asn Glu Leu Gln Glu Leu Glu Gln Phe Gly Cys Pro Thr Cys
 180 185 190
 Gly Ser Cys Ser Gly Met Phe Thr Ala Asn Ser Met Asn Cys Leu Ser
 195 200 205
 Glu Ala Leu Gly Leu Ala Leu Pro Gly Asn Gly Thr Ile Leu Ala Thr
 210 215 220
 Ser Pro Glu Arg Lys Glu Phe Val Arg Lys Ser Ala Ala Gln Leu Met
 225 230 235 240
 Glu Thr Ile Arg Lys Asp Ile Lys Pro Arg Asp Ile Val Thr Val Lys
 245 250 255
 Ala Ile Asp Asn Ala Phe Ala Leu Asp Met Ala Leu Gly Gly Ser Thr
 260 265 270
 Asn Thr Val Leu His Thr Leu Ala Leu Ala Asn Glu Ala Gly Val Glu
 275 280 285
 Tyr Ser Leu Glu Arg Ile Asn Glu Val Ala Glu Arg Val Pro His Leu
 290 295 300
 Ala Lys Leu Ala Pro Ala Ser Asp Val Phe Ile Glu Asp Leu His Glu
 305 310 315 320
 Ala Gly Gly Val Ser Ala Ala Leu Asn Glu Leu Ser Lys Lys Glu Gly
 325 330 335
 Ala Leu His Leu Asp Ala Leu Thr Val Thr Gly Lys Thr Leu Gly Glu
 340 345 350
 Thr Ile Ala Gly His Glu Val Lys Asp Tyr Asp Val Ile His Pro Leu
 355 360 365
 Asp Gln Pro Phe Thr Glu Lys Gly Gly Leu Ala Val Leu Phe Gly Asn
 370 375 380
 Leu Ala Pro Asp Gly Ala Ile Ile Lys Thr Gly Gly Val Gln Asn Gly
 385 390 395 400
 Ile Thr Arg His Glu Gly Pro Ala Val Val Phe Asp Ser Gln Asp Glu
 405 410 415
 Ala Leu Asp Gly Ile Ile Asn Arg Lys Val Lys Glu Gly Asp Val Val
 420 425 430
 Ile Ile Arg Tyr Glu Gly Pro Lys Gly Gly Pro Gly Met Pro Glu Met
 435 440 445
 Leu Ala Pro Thr Ser Glu Ile Val Gly Met Gly Leu Gly Pro Lys Val
 450 455 460
 Ala Leu Ile Thr Asp Gly Arg Ile Ser Gly Ala Ser Arg Gly Leu Ser

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<210> 39
<211> 194
<212> DNA
<213> Artificial Sequence
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<220>
<221> -35 signal
<222> (136)..(141)
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<220>
<221> -10_signal
<222> (159)..(164)
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1400: 39
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 tattttctccc ttgagggggha aaaaagaggtg tccctagaaq agatccagtc ttgtgaaaaa 120
 ttttcaaaaa aggtattgac ttctctcaca aggtgtgtgaa taattttatt aagggagggg 180
 caaacccgcg ctgtc
 194

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

Abstract

$\frac{d}{dt} \left(\frac{\partial L}{\partial \dot{x}} \right) = \frac{\partial L}{\partial x}$

A

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ad

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aj

ak

al

am

an

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aq

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aw

ax

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fv

fw

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fz

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gf

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gh

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gk

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gm

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gq

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gt

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gv

gw

gx

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hp

hq

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<400> 40
ggtacattag attacaagaa agatatttta acagacacaag aggggaaaga tgttttggtt 60
tacatcaga acaactcttg ttaaaatttc tgaaaaattt tgcaaaaagt ttttgacttt 120
atctacaagg tgtgggtataa taattttaac aacagcagga cgc 163

<210> 41
<211> 127
<212> DNA
<213> Artificial Sequence

<220>
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sequence

<220>
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<222> (34)..(39)

<220>
<221> -10_signal
<222> (58)..(63)

<220>
<221> -35_signal
<222> (75)..(80)

<220>
<221> -10_signal
<222> (98)..(103)

<400> 41
gaggaattat agaattttgt caaaataatt ttattgacaa cgttttattt acgttgatat 60
aatttaattt ttatttgaca aaaaatgggt cgtgttgtac aataaatgta gtgaggtgga 120
tgcaatg 127

<210> 42
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome
binding site

<400> 42
taaacattag gaggagaaaa catg 24

<210> 43
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome

binding site

<400> 43
attcgagaaa tyyagagaat ataatatg 29

<210> 44
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome
binding site

<400> 44
agaaaaggagg tga 13

<210> 45
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome
binding site

<220>
<221> misc_feature
<222> 17-20
<223> n = a, c, g, or t

<400> 45
ttaaqaagagg agtgannnn atg 23

<210> 46
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome
binding site

<220>
<221> misc_feature
<222> 16-20
<223> n = a, c, g, or t

<400> 46
ttayaaagga gytgannnn atg 23

<210> 47
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome
binding site

<220>

<221> misc_feature

<222> 14-21

<223> n = a, c, g, or t

<400> 47

agaaaggagg tgannnnnn atg

23

<210> 48

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ribosome
binding site

<220>

<221> misc_feature

<222> 14-19

<223> n = a, c, g, or t

<400> 48

agaaaggagg tgannnnnna tg

22

<210> 49

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ribosome
binding site

<400> 49

actatagaa agaggagaa acatg

25

<210> 50

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ribosome
binding site

<400> 50

actatagag gagagagaa catg

24

<210> 51

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ribosome
binding site

<400> 51

tagagagc gactatg atg

24

<210> 51
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome
binding site

<400> 52
ttagaaagga ggtttaatta atg 23

<210> 53
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome
binding site

<400> 53
ttagaaagga ggtgatttaa atg 23

<210> 54
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome
binding site

<400> 54
ttagaaagga ggtgtttaa atg 23

<210> 55
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome
binding site

<400> 55
attcagaaaa ggaggtgaat ataatat 24

<210> 56
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome
binding site

<400> 56
attcagaaaa ggaggtgaat ataatat 24

<210> 57

<211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: ribosome
 binding site

<400> 57
 atttgtagaa aggaggtaga ttaatatg

25

<210> 58
 <211> 3291
 <212> DNA
 <213> Bacillus subtilis

<400> 58
 atgggggaacta atgtacaggt ggattcagca totgcgaat gtacacagac gatgagcgga 60
 gcattaatgc tgattgaatc attaaaaaaaa gagaaagtag aaatgatcctt cgggttatccg 120
 ggggggggtg tgattccgat ttaacataag ctatataatt caggggttggt acatatacctt 180
 cccgttcacg aacaaggagc aattcagca gaggagggt acgcaagggt cccggaaaa 240
 cgggttgctg taattgcac gtcagggcgc ggagcgacaa acattgttac aggcattgat 300
 gatgcacga ttgattcatt gcgtttagta gtcattacag ggcaggtatc aacctctgta 360
 atcgggagcg atgcatttca ggaagcagac attttaggga ttaacatgac agtcaaaaa 420
 caaggttac aggttcgcga ggcgaaagat ctgtagga taattaaaa agcgttcac 480
 attcaaaaa atggaagac cgggactgta ttgatcgata ttccaaaaa tctagcaaca 540
 attgaaggag aattcagcta cgatcatgag atgaattctc cgggatacca gcgcacaaca 600
 gagcgaatt atttgcagat ccgcgaagctt gtggaaagcg tgagcagtcg gaaaaaacccg 660
 ggcattcctg cgggttcggg cgtactgcac gaaaaacgt cagaagaatt aaaaaattat 720
 gctgaacagc agcaaatccc tctggcacac acccttttgg ggttcggagg ctccccgggt 780
 aaccatccgc tttctcagg gatggcgga atgcacgta ctatataac caatatttt 840
 cttaatgaat gtattctatt aatcagtat cccacccctt ttgtagac tctacagga 900
 aacctgaac acattgcacg aaacgcaag atgacacaa tcatattta tccattctaa 960
 atcgaaaaa taatgaaac aacattttt gtaattgga acatcaaaa tgtctcgaa 1020
 gactatata acaagaaat caaaaaat gattcagat aatcaaaa acaatcgaa 1080
 gactcaaaa acaatatac attcattat gattcatt caaaaagt tctcattat 1140
 caaaattga ttgaattat taattattt acaaaaaa aggcattgt acaattgat 1200
 taattttag atcaattat taattattt caaaaaa aggcattgt acaattgat 1260

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gcacaaagagt ggatcgtcga aaaccaagta aacccgtcctt gtttcaacgc tatcaatgca 3180
 agcgagaaag aacatcaaat cgaagtagtg ggaagaaagc ttctgcaaat gatcccggtt 3240
 gtgaaacaag gcaagaagaa ggaagcggtg gttccggttg gcacaaatta a 3291

<210> 59
 <211> 2363
 <212> DNA
 <213> Bacillus subtilis

<220>
 <221> CDS
 <222> (242)..(1072)

<220>
 <221> CDS
 <222> (1077)..(1934)

<220>
 <221> CDS
 <222> (1939)..(2319)

<400> 59
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 cctattatta aaatagatag acattgcagc agttcgctt gatccaaaaa aggaatggga 120
 cagaggggatg aaactcgcgc aaatttagaa agtgagaagt ccttcctcgtt gtaacqgaag 180
 gtctctttagc tggcagaaga aaacggcaga tcatctcttc caaacatgag gattaaaaa 240
 c atg aaa aca aaa ctg gat ttt cta aaa atg aag gag tct gaa gaa cgc 289
 Met Lys Thr Lys Leu Asp Phe Leu Lys Met Lys Glu Ser Glu Glu Pro
 1 5 10 15

att gtc atg ctg acc gct tat gat tat aag gca gct aaa ctt cct gaa 337
 Ile Val Met Leu Thr Ala Tyr Asp Tyr Pro Ala Ala Lys Leu Ala Glu
 20 25 30

caa gag gga gtt gac atg att tta gtc ggt gat tca ctt gga atg gtc 385
 Gln Ala Gly Val Asp Met Ile Leu Val Gly Asp Ser Leu Gly Met Val
 35 40 45

gta ctg ggt ctt gat tca att gta gtt ctg aca gtt gga gac atg atg 433
 Val Leu Gly Leu Asp Ser Thr Val Gly Val Thr Val Ala Asp Met Ile
 50 55 60

gat gat aca aaa ggc gtt aaa aga ggt gag cct aac aac ttt att tta 481
 His His Thr Lys Ala Val Lys Arg Gly Ala Pro Asn Thr Phe Ile Val
 65 70 75

aca gat gta ggt ttt atg ttt gat gac ctg ttt aag gaa gat att att 529
 Thr Asp Met Phe Phe Met Ser Tyr His Leu Ser Lys Ala Asp Thr Leu
 80 85 90

aaa atg tta ttt gtt att ttt gag gaa att tta ttt ttt tta ttt att 577
 Lys Asn Ala Ala Ala Ile Val Ala Glu Ser Gly Ala Asp Ala Leu Lys
 95 100 105

att	gag	ggg	gga	gaa	ggc	gtg	ttt	gaa	ttc	att	ggc	gga	ttg	acg	att	628
Leu	Gln	Gly	Gly	Gln	Gly	Val	Phe	Gln	Ser	Ile	Arg	Ala	Leu	Thr	Leu	
		118					120					128				
gga	ggc	att	aca	gta	gtc	agt	cac	tta	ggt	ttg	aca	ccg	cag	tca	gtc	673
Gly	Gly	Ile	Pro	Val	Val	Ser	His	Leu	Gly	Leu	Thr	Pro	Gln	Ser	Val	
		130				138					140					
ggc	gta	ctg	ggc	ggc	tat	aaa	gta	cag	ggc	aaa	gac	gaa	aaa	aga	ggc	721
Gly	Val	Leu	Gly	Gly	Tyr	Lys	Val	Gln	Gly	Lys	Asp	Gln	Gln	Ser	Ala	
		148			150					155					160	
aaa	aaa	tta	ata	gaa	gac	agt	ata	aaa	tgc	gaa	gaa	gca	gga	ggt	atg	769
Lys	Lys	Leu	Ile	Gln	Asp	Ser	Ile	Lys	Cys	Gln	Gln	Ala	Gly	Ala	Met	
				168					170					178		
atg	ctt	gtg	tig	gaa	tgt	gtg	ccg	gta	gaa	ctc	aca	gac	aaa	att	ggc	817
Met	Leu	Val	Leu	Gln	Cys	Val	Pro	Ala	Gln	Leu	Thr	Ala	Lys	Ile	Ala	
		180						188					190			
gag	acg	cta	agg	ata	ccg	gtc	att	gga	atc	ggg	ggt	ggg	gtg	aaa	ggg	865
Gln	Thr	Leu	Ser	Ile	Pro	Val	Ile	Gly	Ile	Gly	Ala	Gly	Val	Lys	Ala	
		198				200						208				
gac	gga	caa	gtt	ctc	gtt	tat	cat	gat	att	atc	ggc	cac	ggg	gtt	gag	913
Asp	Gly	Gln	Val	Leu	Val	Tyr	His	Asp	Ile	Ile	Gly	His	Gly	Val	Gln	
		210				218					220					
aga	aca	cat	aaa	ttt	gta	aag	caa	tat	acg	ggc	att	gat	gaa	acc	atc	961
Arg	Thr	Pro	Lys	Phe	Val	Lys	Gln	Tyr	Thr	Arg	Ile	Asp	Gln	Thr	Ile	
		228			230					238					240	
aaa	aca	gta	atc	agg	aga	tat	gtt	cag	gat	tta	aga	caa	gtt	ggt	ttc	1009
Gln	Thr	Ala	Ile	Ser	Gly	Tyr	Val	Gln	Asp	Val	Arg	His	Arg	Ala	Phe	
				248				250						258		
cat	gaa	caa	aag	cat	tcc	ttt	caa	atg	aac	cag	aca	gtg	ctt	gac	ggc	1057
Pro	Gln	Gln	Lys	His	Ser	Phe	Gln	Met	Asn	Gln	Thr	Val	Leu	Asp	Gly	
			260				268						270			
ttg	tac	ggg	gga	aaa	aaag	atg	aga	cag	att	act	gat	att	tca	cag	gtg	1106
Leu	Tyr	Gly	Gly	Lys		Met	Arg	Gln	Ile	Thr	Asp	Ile	Ser	Gln	Leu	
		278					280						288			
aaa	gaa	gcc	ata	aaa	caa	tac	cat	tca	cag	atc	aaa	tca	act	gta	ttt	1154
Lys	Gln	Ala	Ile	Lys	Gln	Tyr	His	Ser	Gln	Gly	Lys	Ser	Ile	Gly	Phe	
		290					298					300				
gtt	cca	aca	ata	ggg	ttt	ctc	cat	gat	gag	cat	tca	aat	tta	gta	gat	1202
Val	Pro	Thr	Met	Gly	Phe	Leu	His	Gln	Gly	His	Leu	Thr	Leu	Ala	Asp	
		308				310					318					

att gag ggt gat gaa ggt ctt gaa gaa aac gtc gga gtc gat att ctt 1346
 Ile Glu Arg Asp Ala Ala Leu Ala Glu Asn Ala Gly Val Asp Ile Leu
 355 360 365

ttt aag cca gat ggt cat gat atg tat ccc ggt gaa aag aat gtc aag 1394
 Phe Thr Pro Asp Ala His Asp Met Tyr Pro Gly Glu Lys Asn Val Thr
 370 375 380

att cat gta gaa aga cgc aca gac gtg tta tgc ggg cgc tca aga gaa 1442
 Ile His Val Glu Arg Arg Thr Asp Val Leu Cys Gly Arg Ser Arg Glu
 385 390 395

gga cat ttt gac ggg gtc ggg atc gta ctc aag aag ctt ttc aat cta 1490
 Gly His Phe Asp Gly Val Ala Ile Val Leu Thr Lys Leu Phe Asn Leu
 400 405 410 415

gtc aag cgg aat cgt gcc tat ttc ggt tta aaa gat ggc cag cag gta 1538
 Val Lys Pro Thr Arg Ala Tyr Phe Gly Leu Lys Asp Ala Glu Glu Val
 420 425 430

got gtt gtt gat ggg tta atc agc gac ttc ttc atg gat att gaa ttg 1586
 Ala Val Val Asp Gly Leu Ile Ser Asp Phe Phe Met Asp Ile Glu Leu
 435 440 445

gtt cct gtc gat aag gtc aga gag gaa gac ggc tta gcc aaa agc tct 1634
 Val Pro Val Asp Thr Val Arg Glu Glu Asp Gly Leu Ala Lys Ser Ser
 450 455 460

cgc aat gta tac tta aca gct gag gaa aga aaa gaa ggc cct aag ctg 1682
 Arg Asn Val Tyr Leu Thr Ala Glu Glu Arg Lys Glu Ala Pro Lys Leu
 465 470 475

tat cgg ggt gtt gaa aca agt ggt gaa att gtr caa gcc ggt gaa aga 1730
 Tyr Arg Ala Leu Glu Thr Ser Ala Glu Leu Val Glu Ala Gly Glu Arg
 480 485 490 495

gat att gaa ggt gtc ata aaa got gra aaa gat atc att gaa aag aat 1778
 Asp Pro Glu Ala Val Ile Lys Ala Ala Lys Asp Ile Ile Glu Thr Thr
 500 505 510

agc gga acc ata gat tat gta gag ctt tat tcc tat cgc gaa ctc gag 1826
 Ser Gly Thr Ile Asp Tyr Val Glu Leu Tyr Ser Tyr Pro Glu Leu Glu
 515 520 525

cct gtc aat gaa att got gga aag atg att ctc got gtt gca gtt got 1874
 Pro Val Asn Glu Ile Ala Gly Lys Met Ile Leu Ala Val Ala Val Ala
 530 535 540

ttt tca aaa cgt cgt tta ata gat aat atc att att gat att cta gta 1922
 Phe Ser Lys Ala Arg Leu Ile Asp Asn Ile Ile Ile Asp Ile Arg Glu
 545 550 555

atg gag aga ata taat atg tat cga ata atg atg agc ggt aat att gat 1970
 Met Glu Arg Ile Met Tyr Arg Thr Met Met Ser Gly Lys Leu His
 560 565 570

agt tta att ttt att gaa tta aa tta att tat atg gaa att att att 1978
 Arg Ala Thr Val Thr Glu Ala Asn Leu Asn Tyr Val Gly Ser Ile Thr
 575 580 585

att tat gaa tat att att att got att gaa att att att att att 1986
 Ile Ile Val Val Ile Ile Ile got Ile Ile Ile Ile Ile Ile Ile Ile Ile
 590 595 600

ile asp glu asp leu ile asp ala val gly met leu pro asn glu lys
 595 600 605
 gta caa att gtg aat aat aat aat gga gaa ggt att gaa acg tat att 2115
 val gln ile val asn asn asn asn gly ala arg leu glu thr tyr ile
 610 615 620
 att cct ggt aaa cgg gga agc ggc gtc ata tgc tta aac ggt gca gcc 2163
 ile pro gly lys arg gly ser gly val ile cys leu asn gly ala ala
 625 630 635
 gca cgc ctt gtg cag gaa gga gat aag gtc att att att ccc tac aaa 2211
 ala arg leu val gln glu gly asp lys val ile ile ile ser tyr lys
 640 645 650
 atg atg tct gat caa gaa ggc gca agc cat gag cgc aaa gtg gat gtt 2259
 met met ser asp gln glu ala ala ser his glu pro lys val ala val
 655 660 665 670
 ctg aat gat caa aac aaa att gaa caa atg ctg ggg aac gaa cca gcc 2307
 leu asn asp gln asn lys ile glu gln met leu gly asn glu pro ala
 675 680 685
 cgt aca att ttg tagaagaaaa gcccccttla cgggggggttt tcttttaaga tttr 2363
 arg thr ile leu
 690

<210> 60
 <211> 293
 <212> PRT
 <213> Bacillus subtilis

<100> 60
 met ser ile ala val ser glu glu glu ala lys ala val glu gly leu
 1 10 15
 asn asp tyr leu ser val glu glu val glu thr ile tyr ile pro leu
 20 25 30
 val arg leu leu his leu his val lys ser ala ala glu arg asn lys
 35 40 45
 his val asn val phe leu lys his pro his ser ala lys ile pro phe
 50 55 60
 ile ile gly ile ala gly ser val ala val gly lys ser thr thr ala
 65 70 75 80
 arg ile leu gln lys leu leu ser arg leu pro asp arg pro lys val
 85 90 95
 ser leu ile thr thr asp gly phe leu phe pro thr ala glu leu lys
 100 105 110
 lys lys asn met met ser arg lys gly phe phe ala ser tyr asp val
 115 120 125
 lys ala leu leu his phe leu asn asp leu lys pro gly lys asp ser
 130 135 140

Val Lys Ala Pro Val Tyr Ser His Leu Thr Tyr Asp Arg Glu Glu Gly
145 150 155 160

Val Phe Glu Val Val Glu Gln Ala Asp Ile Val Ile Ile Glu Gly Ile
165 170 175

Asn Val Leu Gln Ser Pro Thr Leu Glu Asp Asp Arg Glu Asn Pro Arg
180 185 190

Ile Phe Val Ser Asp Phe Phe Asp Phe Ser Ile Tyr Val Asp Ala Glu
195 200 205

Glu Ser Arg Ile Phe Thr Trp Tyr Leu Glu Arg Phe Arg Leu Leu Arg
210 215 220

Glu Thr Ala Phe Gln Asn Pro Asp Ser Tyr Phe His Lys Phe Lys Asp
225 230 235 240

Leu Ser Asp Gln Glu Ala Asp Glu Met Ala Ala Ser Ile Trp Glu Ser
245 250 255

Val Asn Arg Pro Asn Leu Tyr Glu Asn Ile Leu Pro Thr Lys Phe Arg
260 265 270

Ser Asp Leu Ile Leu Arg Lys Gly Asp Gly His Lys Val Glu Glu Val
275 280 285

Leu Val Arg Arg Val
290

<210> 61

<211> 281

<212> FRT

<213> Bacillus subtilis

<100> 61

Met Glu Gly Leu Asn Asp Tyr Leu Ser Val Glu Glu Val Glu Thr Ile
1 5 10 15

Tyr Ile Pro Leu Val Arg Leu Leu His Leu His Val Lys Ser Ala Ala
20 25 30

Glu Arg Asn Lys His Val Asn Val Phe Leu Lys His Pro His Ser Ala
35 40 45

Lys Ile Pro Phe Ile Ile Gly Ile Ala Gly Ser Val Ala Val Gly Lys
50 55 60

Ser Thr Thr Ala Arg Ile Leu Gln Lys Leu Leu Ser Arg Leu Pro Asp
65 70 75 80

Arg Pro Lys Val Ser Leu Ile Thr Thr Asp Gly Phe Leu Phe Pro Thr
85 90 95

Ala Glu Leu Lys Lys Lys Asn Met Met Ser Arg Lys Gly Ile Pro Glu
100 105 110

Ser Tyr Asp Val Lys Ala Leu Leu Glu Phe Leu Asn Asp Leu Lys Ser
115 120 125

Gly Lys Asp Ser Val Lys Ala Pro Val Tyr Ser His Leu Thr Tyr Asp
 130 135 140
 Arg Glu Glu Gly Val Phe Glu Val Val Glu Gln Ala Asp Ile Val Ile
 145 150 155 160
 Ile Glu Gly Ile Asn Val Leu Gln Ser Pro Thr Leu Glu Asp Asp Arg
 165 170 175
 Glu Asn Pro Arg Ile Phe Val Ser Asp Phe Phe Asp Phe Ser Ile Tyr
 180 185 190
 Val Asp Ala Glu Glu Ser Arg Ile Phe Thr Trp Tyr Leu Glu Arg Phe
 195 200 205
 Arg Leu Leu Arg Glu Thr Ala Phe Gln Asn Pro Asp Ser Tyr Phe His
 210 215 220
 Lys Phe Lys Asp Leu Ser Asp Gln Glu Ala Asp Glu Met Ala Ala Ser
 225 230 235 240
 Ile Trp Glu Ser Val Asn Arg Pro Asn Leu Tyr Glu Asn Ile Leu Pro
 245 250 255
 Thr Lys Phe Arg Ser Asp Leu Ile Leu Arg Lys Gly Asp Gly His Lys
 260 265 270
 Val Glu Glu Val Leu Val Arg Arg Val
 275 280

<210> 62

<211> 1092

<212> DNA

<213> *Bacillus subtilis*

<220>

<221> CDS

<222> (1)..(1089)

<400> 62

atg aat aaa caa aca att cga gtt gaa ttg aca tca aca aaa aaa cgg	48
Met Thr Lys Gln Thr Ile Arg Val Glu Leu Thr Ser Thr Lys Lys Pro	
1 5 10 15	
aaa caa gac caa aat cag att cgg ttc gga aga gtg ttt aca gac cac	96
Lys Pro Asp Pro Asn Gln Leu Ser Phe Gly Arg Val Phe Thr Asp His	
20 25 30	
atg ttt gta atg gac tat gcc gca gat aaa ggt cgg cac gat cca aga	144
Met Phe Val Met Asp Tyr Ala Ala Asp Lys Gly Trp Tyr Asp Pro Arg	
35 40 45	
atc att cat tat caa ccc tta taa atg gat cca aat gga atg atc tat	192
Ile Ile Pro Tyr Gln Pro Leu Ser Met Asp Pro Thr Ala Met Val Tyr	
50 55 60	
taa taa ggc caa atc ggt ttt gaa ccc tta aat ggt taa gta taa gat	240
His Tyr Gly Gln Thr Val Phe Gln Gly Leu Lys Ala Tyr Val Ser Gln	
65 70 75	

gat gac cat gtt ctg ctt ttc aga ccg gaa aaa aat atg gaa cgc ctg	288
Asp Asp His Val Leu Leu Phe Arg Pro Glu Lys Asn Met Glu Arg Leu	
85 90 95	
aat caa tca aac gac cgc ctg tgc atc ccg caa att gat gaa gaa gag	336
Asn Gln Ser Asn Asp Arg Leu Cys Ile Pro Gln Ile Asp Glu Glu Gln	
100 105 110	
gtt ctt gaa ggc tta aag cag ctt gtc gca att gat aaa gac tgg att	384
Val Leu Glu Gly Leu Lys Gln Leu Val Ala Ile Asp Lys Asp Trp Ile	
115 120 125	
cca aat gcg gag ggc acg tcc ctt tac atc cgt ccg ttc atc atc gca	432
Pro Asn Ala Glu Gly Thr Ser Leu Tyr Ile Arg Pro Phe Ile Ile Ala	
130 135 140	
acc gag cct ttc ctt ggt gtt gcg gca tct cat acg tat aag ctg ttg	480
Thr Glu Pro Phe Leu Gly Val Ala Ala Ser His Thr Tyr Lys Leu Leu	
145 150 155 160	
atc att ctt tct ccg gtc ggc tct tat tac aaa gaa ggc att aag ccg	528
Ile Ile Leu Ser Pro Val Gly Ser Tyr Tyr Lys Glu Gly Ile Lys Pro	
165 170 175	
gtc aaa atc got gtt gaa agt gaa ttc gtc cgt gcg gta aaa ggc gga	576
Val Lys Ile Ala Val Glu Ser Glu Phe Val Arg Ala Val Lys Gly Gly	
180 185 190	
aca gga aat gcc aaa acc gca gga aac tat got tca agc tta aaa gcg	624
Thr Gly Asn Ala Lys Thr Ala Gly Asn Tyr Ala Ser Ser Leu Lys Ala	
195 200 205	
cag cag gta gcc gaa gag aaa gga ttt tct caa gta ctg tgg ctg gac	672
Gln Gln Val Ala Glu Glu Lys Gly Phe Ser Gln Val Leu Trp Leu Asp	
210 215 220	
ggc att gag aag aaa tac atc gaa gaa gtc gga agc atg aac atc ttc	720
Gly Ile Glu Lys Lys Tyr Ile Glu Glu Val Gly Ser Met Asn Ile Phe	
225 230 235 240	
ttc aaa atc aac ggt gaa atc gta aca ccg atg ctg aac ggc aat atc	768
Phe Lys Ile Asn Gly Glu Ile Val Thr Pro Met Leu Asn Gly Ser Ile	
245 250 255	
ctg gaa ggc att acg cgc aat tca gtc atc gcc ttg ctt aag cat tgg	816
Leu Glu Gly Ile Thr Arg Asn Ser Val Ile Ala Leu Leu Lys His Trp	
260 265 270	
ggc att caa gtt tca gaa cga aaa att gcg atc gat gag ctg atc caa	864
Gly Leu Gln Val Ser Glu Arg Lys Ile Ala Ile Asp Glu Val Ile Gln	
275 280 285	
gcc cat aaa gac gtc atc ctg aaa gaa gcc ttc gga aca ggt aca gca	912
Ala His Lys Asp Gly Ile Leu Glu Gln Ala Phe Gly Thr Gly Thr Ala	
290 295 300 305	
ggt gtt att tca tca ttc ggt gag gtc atc tgg caa caa tta atc ctt	960
Ala Val Ile Ser Pro Val Gly Glu Leu Ile Trp Gln Asp His Thr Leu	
310 315 320	
tat att att att att tta aaa gaa gaa gaa gaa gaa gaa gaa gaa	1008

Ser Ile Asn Asn Gly Glu Thr Gly Glu Ile Ala Lys Lys Leu Tyr Asp
 325 330 335

acg att aca ggc att caa aaa ggc gct gtc gca gac gaa ttc gga tgg 1086
 Thr Ile Thr Gly Ile Gln Lys Gly Ala Val Ala Asp Glu Phe Gly Trp
 340 345 350

acg acc gaa gtc gca ggc ctg act gaa agc aag taa 1092
 Thr Thr Glu Val Ala Ala Leu Thr Glu Ser Lys
 355 360

<210> 63
 <211> 363
 <212> PRT
 <213> Bacillus subtilis

<400> 63
 Met Thr Lys Gln Thr Ile Arg Val Glu Leu Thr Ser Thr Lys Lys Pro
 1 5 10 15

Lys Pro Asp Pro Asn Gln Leu Ser Phe Gly Arg Val Phe Thr Asp His
 20 25 30

Met Phe Val Met Asp Tyr Ala Ala Asp Lys Gly Trp Tyr Asp Pro Arg
 35 40 45

Ile Ile Pro Tyr Gln Pro Leu Ser Met Asp Pro Thr Ala Met Val Tyr
 50 55 60

His Tyr Gly Gln Thr Val Phe Glu Gly Leu Lys Ala Tyr Val Ser Glu
 65 70 75 80

Asp Asp His Val Leu Leu Phe Arg Pro Glu Lys Asn Met Glu Arg Leu
 85 90 95

Asn Gln Ser Asn Asp Arg Leu Cys Ile Pro Gln Ile Asp Glu Glu Gln
 100 105 110

Val Leu Glu Gly Leu Lys Gln Leu Val Ala Ile Asp Lys Asp Trp Ile
 115 120 125

Pro Asn Ala Glu Gly Thr Ser Leu Tyr Ile Arg Pro Phe Ile Ile Ala
 130 135 140

Thr Glu Pro Phe Leu Gly Val Ala Ala Ser His Thr Tyr Lys Leu Leu
 145 150 155 160

Ile Ile Leu Ser Pro Val Gly Ser Tyr Tyr Lys Glu Gly Ile Lys Pro
 165 170 175

Val Lys Ile Ala Val Glu Ser Glu Phe Val Arg Ala Val Lys Gly Gly
 180 185 190

Thr Gly Asn Ala Lys Thr Ala Gly Asn Tyr Ala Ser Ser Leu Lys Ala
 195 200 205

Gln Gln Val Ala Gln Gln Lys Gly Phe Ser Gln Val Leu Trp Leu Asp
 210 215 220

Gly Ile Gln Lys Lys Tyr Ile Gln Gln Val Gly Ser Met Asn Ile Phe

225	230	235	240
Phe Lys Ile Asn Gly Glu Ile Val Thr Pro Met Leu Asn Gly Ser Ile			
245	250	255	
Leu Glu Gly Ile Thr Arg Asn Ser Val Ile Ala Leu Leu Lys His Trp			
260	265	270	
Gly Leu Gln Val Ser Glu Arg Lys Ile Ala Ile Asp Glu Val Ile Gln			
275	280	285	
Ala His Lys Asp Gly Ile Leu Glu Glu Ala Phe Gly Thr Gly Thr Ala			
290	295	300	
Ala Val Ile Ser Pro Val Gly Glu Leu Ile Trp Gln Asp Glu Thr Leu			
305	310	315	320
Ser Ile Asn Asn Gly Glu Thr Gly Glu Ile Ala Lys Lys Leu Tyr Asp			
325	330	335	
Thr Ile Thr Gly Ile Gln Lys Gly Ala Val Ala Asp Glu Phe Gly Trp			
340	345	350	
Thr Thr Glu Val Ala Ala Leu Thr Glu Ser Lys			
355	360		

<210> 64
 <211> 1071
 <212> DNA
 <213> Bacillus subtilis

<220>
 <221> CDS
 <222> (1)..(1064)

<400> 64	
ttg aat aag att att gaa cga gaa aaa act gta tat tat aag gaa aag	48
Met Asn Lys Leu Ile Glu Arg Glu Lys Thr Val Tyr Tyr Lys Glu Lys	
1 5 10 15	
ccc gac cag tat tcc ttg ggg ttc gga caa tat ttc aca gat tat atg	96
Pro Asp Pro Ser Ser Leu Gly Phe Gly Gln Tyr Phe Thr Asp Tyr Met	
20 25 30	
ttt gtg atg gac tac gaa gag ggg att gga tgg cat cat cag aga att	144
Phe Val Met Asp Tyr Glu Glu Gly Ile Gly Tyr His His Pro Arg Ile	
35 40 45	
ggg cag tac gca cag att acg att gat cag tat tca tct gtt ttt cat	192
Ala Pro Tyr Ala Pro Leu Thr Leu Asp Pro Ser Ser Ser Val Phe His	
50 55 60	
tac ggt cag gtt gtt ttt gaa gga tta aaa gga tac gaa gca gac gac	240
Tyr Gly Gln Ala Val Phe Gln Gly Leu Lys Ala Tyr Arg Thr Asp Asp	
65 70 75 80	
ttt agt atg tat ttt ttt ttt ggt ttt tat gaa att att aat ttt gtt tat	288
Gly Arg Val Leu Leu Leu Phe Arg Pro Asp Gln Asn Ile Lys Arg Leu Asn	
85 90 95	

Thr Ile Thr Asp Ile Gln Leu Gly Lys Val Lys Gly Pro Phe Asn Trp
 340 345 350

aca ggg gaa ggg tga
 Thr Val Glu Val
 355

1071

<210> 65
 <211> 356
 <212> PRT
 <213> Bacillus subtilis

<400> 65
 Met Asn Lys Leu Ile Gln Arg Glu Lys Thr Val Tyr Tyr Lys Glu Lys
 1 5 10 15

Pro Asp Pro Ser Ser Leu Gly Phe Gly Gln Tyr Phe Thr Asp Tyr Met
 20 25 30

Phe Val Met Asp Tyr Glu Glu Gly Ile Gly Trp His His Pro Arg Ile
 35 40 45

Ala Pro Tyr Ala Pro Leu Thr Leu Asp Pro Ser Ser Ser Val Phe His
 50 55 60

Tyr Gly Gln Ala Val Phe Glu Gly Leu Lys Ala Tyr Arg Thr Asp Asp
 65 70 75 80

Gly Arg Val Leu Leu Phe Arg Pro Asp Gln Asn Ile Lys Arg Leu Asn
 85 90 95

Arg Ser Cys Glu Arg Met Ser Met Pro Pro Leu Asp Glu Glu Leu Val
 100 105 110

Leu Glu Ala Leu Thr Gln Leu Val Glu Leu Glu Lys Asp Trp Val Pro
 115 120 125

Lys Glu Lys Gly Thr Ser Leu Tyr Ile Arg Pro Phe Val Ile Ala Thr
 130 135 140

Glu Pro Ser Leu Gly Val Lys Ala Ser Arg Ser Tyr Thr Phe Met Ile
 145 150 155 160

Val Leu Ser Pro Val Gly Ser Tyr Tyr Gly Asp Asp Gln Leu Lys Pro
 165 170 175

Val Arg Ile Tyr Val Glu Asp Glu Tyr Val Arg Ala Val Asn Gly Gly
 180 185 190

Val Gly Phe Ala Lys Thr Ala Gly Asn Tyr Ala Ala Ser Leu Gln Ala
 195 200 205

Gln Arg Lys Ala Asn Glu Leu Gly Tyr Asp Gln Val Leu Trp Leu Asp
 210 215 220

Ala Ile Ala Lys Lys Tyr Val Glu Glu Val Gly Ser Met Asn Ile Phe
 225 230 235 240

Phe Val Ile Asn Gly Glu Ala Val Thr Pro Ala Leu Asn Gly Ser Ile
 245 250

Leu Ser Gly Val Thr Arg Ala Ser Ala Ile Glu Leu Ile Arg Ser Trp
260 265 270

Gly Ile Pro Val Arg Glu Glu Arg Ile Ser Ile Asp Glu Val Tyr Ala
275 280 285

Ala Ser Ala Arg Gly Glu Leu Thr Glu Val Phe Gly Thr Gly Thr Ala
290 295 300

Ala Val Val Thr Pro Val Gly Glu Leu Asn Ile His Gly Lys Thr Val
305 310 315 320

Ile Val Gly Asp Gly Gln Ile Gly Asp Leu Ser Lys Lys Leu Tyr Glu
325 330 335

Thr Ile Thr Asp Ile Gln Leu Gly Lys Val Lys Gly Pro Phe Asn Trp
340 345 350

Thr Val Glu Val
355

<210> 66

<211> 1428

<212> DNA

<213> Bacillus subtilis

<220>

<221> CDS

<222> (1)...(1428)

<400> 66

atg tta aac ggc caa aaa gaa tat cta gtc gaa aaa gac ttc att att 4-
Met Leu Asn Gly Gln Lys Glu Tyr Arg Val Glu Lys Asp Phe Leu Gly
1 5 10 15

gaa aaa caa att gaa gca gat gtt tat tac gga att cag acg ctc cgt 96
Glu Lys Gln Ile Glu Ala Asp Val Tyr Tyr Gly Ile Gln Thr Leu Arg
20 25 30

gct tct gaa aat ttt ccg atc aca gga tac aaa atc cat gag gaa atg 144
Ala Ser Glu Asn Phe Pro Ile Thr Gly Tyr Lys Ile His Glu Glu Met
35 40 45

att aac gaa ctg ggc att atg aaa aaa ggt gaa gct att gac aac atg 192
Ile Asn Ala Leu Ala Ile Val Lys Lys Ala Ala Ala Leu Ala Asn Met
50 55 60

gac atg aaa cag ctg tat gaa gga att ggc caa gct atc ata caa ggt 240
Asp Val Lys Arg Leu Tyr Glu Gly Ile Gly Gln Ala Ile Val Gln Ala
65 70 75 80

gct tat aac att ctg gaa ttc att ttt cat gat caa att ttc ttc ggt 288
Ala Asp Ala Ile Leu Ala Gly Lys Trp His Asp Gln Phe Ile Val Asp
85 90 95

atg att tat ggt ggt ggt gga att ttt att aac att aac att att att 336
Ile Ile Gln Gly Gly Ala Gly Thr Ser Met Asn Met Asn Ala Asn Gln
100 105 110 115

Ala Ser Glu Ala Gly Gln Leu Glu Leu Asn Val Met Glu Pro Val Leu
355 360 365

gtc ttt aat ttg ctt caa tcc atc agc atc atg aac aac ggc ttc cgt 1152
Val Phe Asn Leu Leu Gln Ser Ile Ser Ile Met Asn Asn Gly Phe Arg
370 375 380

tgg ttc aat gac aac tgc tta aaa ggc att gaa ggc aac gaa aag cgt 1200
Ser Phe Thr Asp Asn Cys Leu Lys Gly Ile Glu Ala Asn Glu Lys Arg
385 390 395 400

atg aag caa tac gta gaa aaa agc gaa ggc gtg atc aca gct gtc aat 1248
Met Lys Gln Tyr Val Glu Lys Ser Ala Gly Val Ile Thr Ala Val Asn
405 410 415

cgc cat ctt ggg tat gaa gag gaa gat aga att gcc agc gaa gca att 1296
Pro His Leu Gly Tyr Glu Ala Ala Ala Arg Ile Ala Arg Glu Ala Ile
420 425 430

atg aca ggg caa tct gtc cgg gat ctt tgt ctg cag cat gat gtg ctg 1344
Met Thr Gly Gln Ser Val Arg Asp Leu Cys Leu Gln His Asp Val Leu
435 440 445

aat gaa gaa gaa ttg gat att att tta aac cca tat gag atg acc aaa 1392
Thr Glu Glu Glu Leu Asp Ile Ile Leu Asn Pro Tyr Glu Met Thr Lys
450 455 460

cca ggt atc gca ggg aaa gaa tta tta gaa aaa taa 1428
Pro Gly Ile Ala Gly Lys Glu Leu Leu Glu Lys
465 470 475

<210> 67
<211> 475
<212> FRT
<213> *Bacillus subtilis*

<400> 67
Met Leu Asn Gly Gln Lys Glu Tyr Arg Val Glu Lys Asp Phe Leu Gly
1 5 10 15

Glu Lys Gln Ile Glu Ala Asp Val Tyr Tyr Gly Ile Gln Thr Leu Arg
20 25 30

Ala Ser Glu Asn Phe Pro Ile Thr Gly Tyr Lys Ile His Glu Glu Met
35 40 45

Ile Asn Ala Leu Ala Ile Val Lys Lys Ala Ala Ala Leu Ala Asn Met
50 55 60

Asp Val Lys Arg Leu Tyr Glu Gly Ile Gly Gln Ala Ile Val Gln Ala
65 70 75 80

Ala Asp Glu Ile Leu Glu Gly Lys Tyr His Asp Gln Phe Ile Val Asp
85 90 95 100

Pr Ile Ala Gly Gly Ala Gly Thr Ser Met Asn Met Asn Ala Asn Ala
105 110 115 120 125

Val Ile Gly Asn Arg Ala Leu Glu Ile Met Gly His Lys Lys Gly Asn
130 135 140 145 150

Tyr Ile His Leu Ser Pro Asn Thr His Val Asn Met Ser Gln Ser Gln
 130 135 140
 Asn Asp Val Phe Pro Thr Ala Ile His Ile Ser Thr Leu Lys Leu Leu
 145 150 155 160
 Glu Lys Leu Leu Lys Thr Met Glu Asp Met His Ser Val Phe Lys Gln
 165 170 175
 Lys Ala Gln Glu Phe His Ser Val Ile Lys Met Gly Arg Thr His Leu
 180 185 190
 Gln Asp Ala Val Pro Ile Arg Leu Gly Gln Glu Phe Glu Ala Tyr Ser
 195 200 205
 Arg Val Leu Glu Arg Asp Ile Lys Arg Ile Lys Gln Ser Arg Gln His
 210 215 220
 Leu Tyr Glu Val Asn Met Gly Ala Thr Ala Val Gly Thr Gly Leu Asn
 225 230 235 240
 Ala Asp Pro Glu Tyr Ile Lys Gln Val Val Lys His Leu Ala Asp Ile
 245 250 255
 Ser Gly Leu Pro Leu Val Gly Ala Asp His Leu Val Asp Ala Thr Gln
 260 265 270
 Asn Thr Asp Ala Tyr Thr Glu Val Ser Ala Ser Leu Lys Val Cys Met
 275 280 285
 Met Asn Met Ser Lys Ile Ala Asn Asp Leu Arg Leu Met Ala Ser Gly
 290 295 300
 Pro Arg Ala Gly Leu Ala Glu Ile Ser Leu Pro Ala Arg Gln Pro Gly
 305 310 315 320
 Ser Ser Ile Met Pro Gly Lys Val Asn Pro Val Met Ala Glu Leu Ile
 325 330 335
 Asn Gln Ile Ala Phe Gln Val Ile Gly Asn Asp Asn Thr Ile Cys Leu
 340 345 350
 Ala Ser Glu Ala Gly Gln Leu Glu Leu Asn Val Met Glu Pro Val Leu
 355 360 365
 Val Phe Asn Leu Leu Gln Ser Ile Ser Ile Met Asn Asn Gly Phe Arg
 370 375 380
 Ser Phe Thr Asp Asn Cys Leu Lys Gly Ile Glu Ala Asn Gln Lys Arg
 385 390 395 400
 Met Lys Gln Tyr Val Glu Lys Ser Ala Gly Val Ile Thr Ala Val Asn
 405 410 415
 Pro His Leu Gly Tyr Glu Ala Ala Ala Arg Ile Ala Arg Glu Ala Ile
 420 425 430
 Met Thr Gly Gln Ser Val Arg Asp Leu Lys Leu His His Asp Val Leu
 435 440 445

Thr Glu Glu Glu Leu Asp Ile Ile Leu Asn Pro Tyr Glu Met Thr Lys
450 455 460

Pro Gly Ile Ala Gly Lys Glu Leu Leu Glu Lys
465 470 475

<210> 68

<211> 768

<212> DNA

<213> Bacillus subtilis

<220>

<221> CDS

<222> (1)..(768)

<400> 68

atg aaa gga gaa agc aac att caa ggc ctc agc cgt ggt caa aaa gat 45
Met Lys Arg Glu Ser Asn Ile Gln Val Leu Ser Arg Gly Gln Lys Asp
1 5 10 15

cag cct gtg agc cag att tat caa gta tca aca atg aat tct cta tta 96
Gln Pro Val Ser Gln Ile Tyr Gln Val Ser Thr Met Thr Ser Leu Leu
20 25 30

gac gga gta tat gac gga gat ttt gaa ctg tca gag att ccg aaa tat 144
Asp Gly Val Tyr Asp Gly Asp Phe Glu Leu Ser Glu Ile Pro Lys Tyr
35 40 45

gga gac ttc ggt atc gga acc ttt aac aag ctt gac gga gag ctg att 192
Gly Asp Phe Gly Ile Gly Thr Phe Asn Lys Leu Asp Gly Glu Leu Ile
50 55 60

ggg ttt gac ggc gaa ttt tac cgt att agc tca gac gga acc ggc gca 240
Gly Phe Asp Gly Glu Phe Tyr Arg Leu Arg Ser Asp Gly Thr Ala Thr
65 70 75 80

ccg gtc caa aat gga gac cgt tca ccg ttc tgt tca ttt acg ttc ttt 288
Pro Val Gln Asn Gly Asp Arg Ser Pro Phe Cys Ser Phe Thr Phe Phe
85 90 95

aca ccg gac atg acc cac aaa att gat gcg aaa atg aca cgc gaa gac 336
Thr Pro Asp Met Thr His Lys Ile Asp Ala Lys Met Thr Arg Glu Asp
100 105 110

ttt gaa aaa gag atc aac aac atg ctg cca acc aga aac tta ttt tat 384
Phe Glu Lys Glu Ile Asn Ser Met Leu Pro Ser Arg Asn Leu Phe Tyr
115 120 125

gca att cgc att gac gga ttg ttt aaa aat atg cag aca ata aga gta 432
Ala Ile Arg Ile Asp Gly Leu Phe Lys Lys Val Gln Thr Arg Thr Val
130 135 140

aaa ctt gaa gaa aaa ccc tac ttc cca att ttt aaa ccc ttc aaa aca 480
Ala Leu Gln Glu Lys Pro Tyr Val Pro Met Val Glu Ala Val Lys Thr
145 150 155 160

tat ttt att ttt att ttt ttt ttt ttt ttt ttt att tta ttt ttt 528
Ala Trp Ile Ile Asn Phe Asp Asn Val Arg Gly Thr Ile Val Gly Phe
165 170 175 180

ttg aca cca ggt tat gca aac gga atc gcc gtt tct ggc tat cac atg 576
 Leu Thr Pro Ala Tyr Ala Asn Gly Ile Ala Val Ser Gly Tyr His Leu
 180 185 190

cac ttc att gat gaa gga cgc aat tca gcc gga cac gtt ttt gac tat 624
 His Phe Ile Asp Glu Gly Arg Asn Ser Gly Gly His Val Phe Asp Tyr
 195 200 205

gtg ctt gag gat tgc acg gtt acg att tct caa aaa atg aac atg aat 672
 Val Leu Glu Asp Cys Thr Val Thr Ile Ser Gln Lys Met Asn Met Asn
 210 215 220

ctc aga ctt cgg aac aca ggc gat ttc ttt aat gag aat ctg gat aac 720
 Leu Arg Leu Pro Asn Thr Ala Asp Phe Phe Asn Ala Asn Leu Asp Asn
 225 230 235 240

cct gat ttt ggc aaa gat atc gaa aca aat gaa gga acc cct gaa taa 768
 Pro Asp Phe Ala Lys Asp Ile Glu Thr Thr Glu Gly Ser Pro Glu
 245 250 255

<210> 69

<211> 255

<212> PRT

<213> Bacillus subtilis

<400> 69

Met Lys Arg Glu Ser Asn Ile Gln Val Leu Ser Arg Gly Gln Lys Asp
 1 5 10 15

Gln Pro Val Ser Gln Ile Tyr Gln Val Ser Thr Met Thr Ser Leu Leu
 20 25 30

Asp Gly Val Tyr Asp Gly Asp Phe Glu Leu Ser Glu Ile Pro Lys Tyr
 35 40 45

Gly Asp Phe Gly Ile Gly Thr Phe Asn Lys Leu Asp Gly Glu Leu Ile
 50 55 60

Gly Phe Asp Gly Glu Phe Tyr Arg Leu Arg Ser Asp Gly Thr Ala Thr
 65 70 75 80

Pro Val Gln Asn Gly Asp Arg Ser Pro Phe Cys Ser Phe Thr Phe Phe
 85 90 95

Thr Pro Asp Met Thr His Lys Ile Asp Ala Lys Met Thr Arg Glu Asp
 100 105 110

Phe Gln Lys Glu Ile Asn Ser Met Leu Pro Ser Arg Asn Leu Phe Tyr
 115 120 125

Ala Ile Arg Ile Asp Gly Leu Phe Lys Lys Val Gln Thr Arg Thr Val
 130 135 140

Gln Leu Gln Gln Lys Pro Tyr Val Pro Met Val Glu Ala Val Lys Thr
 145 150 155 160

Gln Pro Ile Phe Asn Phe Asp Asn Val Arg Gly Thr Ile Val Gly Phe
 165 170 175

Leu Thr Pro Ala Tyr Ala Asn Gly Ile Ala Val Ser Gly Tyr His Leu

180	185	190
His Phe Ile Asp Glu Gly Arg Asn Ser Gly Gly His Val Phe Asp Tyr		
195	200	205
Val Leu Glu Asp Cys Thr Val Thr Ile Ser Glu Lys Met Asn Met Asn		
210	215	220
Leu Arg Leu Pro Asn Thr Ala Asp Phe Phe Asn Ala Asn Leu Asp Asn		
225	230	235
Pro Asp Phe Ala Lys Asp Ile Glu Thr Thr Glu Gly Ser Pro Glu		
245	250	255

<210> 70

<211> 1254

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)..(1251)

<400> 70

atg aca ttc tcc ctt ttt ggt gac aaa ttt acc cgc cac tcc ggc att	48
Met Thr Phe Ser Leu Phe Gly Asp Lys Phe Thr Arg His Ser Gly Ile	
1 5 10 15	
acg ctg ttg atg gaa gat ctg aac gac ggt tta cgc acg cct ggc gcg	96
Thr Leu Leu Met Glu Asp Leu Asn Asp Gly Leu Arg Thr Pro Gly Ala	
20 25 30	
att atg ctc ggc ggc ggt aat cgc gcg cag atc cgc gaa atg cag gac	144
Ile Met Leu Gly Gly Gly Asn Pro Ala Gln Ile Pro Glu Met Gln Asp	
35 40 45	
tac ttc cag acg cta ctg acc gac atg ctg gaa agt ggc aaa gcg act	192
Tyr Phe Gln Thr Leu Leu Thr Asp Met Leu Glu Ser Gly Lys Ala Thr	
50 55 60	
gat gca ctg tgt aac tac gac ggt cca cag ggc aaa acg gag cta ctc	240
Asp Ala Leu Cys Asn Tyr Asp Gly Pro Gln Gly Lys Thr Glu Leu Leu	
65 70 75 80	
aca ctg ctt ggc gga atg ctg cgc gag aag ttg agt cag gat atc gaa	288
Thr Leu Leu Ala Gly Met Leu Arg Glu Lys Leu Gly Tyr Asp Ile Glu	
85 90 95	
cca cag aat att gca cta aca aac ggc agc cag acc gcg ctt ctc tac	336
Pro Gln Asn Ile Ala Leu Thr Asn Gly Ser Gln Ser Ala Phe Phe Tyr	
100 105 110	
tta ttt aat ctg ttt cgc gga cgc ggt gcc tat tat cgc att aaa aaa	384
Leu Phe Asn Leu Phe Ala Gly Arg Arg Ala Asp Gly Arg Val Lys Lys	
115 120 125	
tta tta tta cag att cca att tat tat att tat att tat att att	432
Val Leu Phe Pro Leu Ala Pro Ala Tyr Ile Gly Tyr Ala Asp Ala Gly	
135 140 145	

ctg gaa gaa gat ctg ttt gtc tat gag cgt cag aat att gaa ctg ctg	480
Leu Glu Glu Asp Leu Phe Val Ser Ala Arg Pro Asn Ile Glu Leu Leu	
145 150 155 160	
cag gaa ggc cag ttt aaa tac cac gtc gat ttt gag cat ctg cat att	528
Pro Glu Gly Glu Phe Lys Tyr His Val Asp Phe Glu His Leu His Ile	
165 170 175	
ggc gaa gaa acc ggg atg att tgc gtc tcc cgg cag aag aat cca aca	576
Gly Glu Glu Thr Gly Met Ile Cys Val Ser Arg Pro Thr Asn Pro Thr	
180 185 190	
ggc aat gtg att acc gac gaa gag ttg ctg aag ctt gac ggc ctg ggc	624
Gly Asn Val Ile Thr Asp Glu Glu Leu Leu Lys Leu Asp Ala Leu Gly	
195 200 205	
aat caa cac ggc att cag ctg gtg att gat aac gct tat ggc gtc cag	672
Asn Glu His Gly Ile Pro Leu Val Ile Asp Asn Ala Tyr Gly Val Pro	
210 215 220	
ttc cag ggt atc atc ttc agt gaa ggc cgc cag cta tgg aat cag aat	720
Phe Pro Gly Ile Ile Phe Ser Glu Ala Arg Pro Leu Trp Asn Pro Asn	
225 230 235 240	
atc gtg ctg tgc atg agt ctt tcc aag ctg ggt cta cat ggc tcc cgc	768
Ile Val Leu Cys Met Ser Leu Ser Lys Leu Gly Leu Pro Gly Ser Arg	
245 250 255	
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atg aac ggc att atc agc ctg gca cat ggc ggt att ggt cag tgg atg	864
Met Asn Gly Ile Ile Ser Leu Ala Pro Gly Gly Ile Gly Pro Ala Met	
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atg tgr gaa atg att aag cgt aac gat ctg ctg cgc ctg tct gaa aca	912
Met Cys Glu Met Ile Lys Arg Asn Asp Leu Leu Arg Leu Ser Glu Thr	
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gtc acc aaa cag ttt tac tac cag cgt gtt cag gaa act atc ggc atc	960
Val Ile Lys Pro Phe Tyr Tyr Gln Arg Val Gln Glu Thr Ile Ala Ile	
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Ile Arg Arg Tyr Leu Pro Glu Asn Arg Pys Leu Ile His Lys Pro Glu	
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gaa gcc att ttc ctc tgg cta tgg ttt aag gat ttg ccc att aag acc	1056
Gly Ala Ile Phe Leu Trp Leu Trp Phe Lys Asp Leu Pro Ile Thr Thr	
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Lys Glu Leu Tyr Gln Arg Leu Lys Ala Arg Gly Val Leu Met Val Pro	
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Gly His Asn Phe Phe Pro Gly Leu Asp Lys Pro Trp Pro His Thr His	
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Gln Cys Met Arg Met Asn Tyr Val Pro Glu Pro Glu Lys Ile Glu Ala
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Ile Met Leu Gly Gly Gly Asn Pro Ala Gln Ile Pro Glu Met Gln Asp
 35 40 45

Tyr Phe Gln Thr Leu Leu Thr Asp Met Leu Glu Ser Gly Lys Ala Thr
 50 55 60

Asp Ala Leu Cys Asn Tyr Asp Gly Pro Gln Gly Lys Thr Glu Leu Leu
 65 70 75 80

Thr Leu Leu Ala Gly Met Leu Arg Glu Lys Leu Gly Trp Asp Ile Glu
 85 90 95

Pro Gln Asn Ile Ala Leu Thr Asn Gly Ser Gln Ser Ala Phe Phe Tyr
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Leu Phe Asn Leu Phe Ala Gly Arg Arg Ala Asp Gly Arg Val Lys Lys
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Val Leu Phe Pro Leu Ala Pro Glu Tyr Ile Gly Tyr Ala Asp Ala Gly
 130 135 140

Leu Glu Glu Asp Leu Phe Val Ser Ala Arg Pro Asn Ile Glu Leu Leu
 145 150 155 160

Pro Glu Gly Gln Phe Lys Tyr His Val Asp Phe Glu His Leu His Ile
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Gly Glu Glu Thr Gly Met Ile Cys Val Ser Arg Pro Thr Asn Pro Thr
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Gly Asn Val Ile Thr Asp Gln Gln Leu Leu Lys Leu Asp Ala Leu Gly
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Asn Gln His Gly Ile Pro Leu Val Ile Asp Asn Ala Tyr Gly Val Pro
 210 215 220

Phe Pro Gly Ile Ile Phe Ser Gln Ala Arg Pro Leu Thr Asn Pro Asn
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Ile Val Leu Cys Met Ser Leu Ser Lys Leu Gly Leu Pro Gly Ser Arg
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Cys Gly Ile Ile Ile Ala Asn Glu Lys Ile Ile Thr Ala Ile Thr Asn
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Met Asn Gly Ile Ile Ser Leu Ala Pro Gly Gly Ile Gly Pro Ala Met
 275 280 285

Met Cys Glu Met Ile Lys Arg Asn Asp Leu Leu Arg Leu Ser Glu Thr
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Val Ile Lys Pro Phe Tyr Tyr Gln Arg Val Gln Glu Thr Ile Ala Ile
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Ile Arg Arg Tyr Leu Pro Glu Asn Arg Cys Leu Ile His Lys Pro Glu
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Gly Ala Ile Phe Leu Trp Leu Trp Phe Lys Asp Leu Pro Ile Thr Thr
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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Recombinant
pAN196 plasmid

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<223> Description of Artificial Sequence: Recombinant
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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Recombinant
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 atagtcctgt cgggttttgc caccactgac ttgagcgtca gatctctgga tctttgtcag 4140
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 <212> DNA
 <213> *Bacillus subtilis*

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 tat tat tat gga aaa tta gaa tat cac tgg cgt ata gaa aca ago agg 96
 Tyr His Asp Gly Lys Leu Glu Tyr His Trp Arg Ile Glu Thr Ser Arg
 20 25 30
 cat aaa aca gaa gat gag ttt ggg atg att ttg aga tcc tta ttt gat 144
 His Lys Thr Glu Asp Glu Phe Gly Met Ile Leu Arg Ser Leu Phe Asp
 35 40 45
 caa tcc gga ctt atg ttt gaa cag ata gat ggc att att att tgg tca 192
 His Ser Gly Leu Met Phe Glu Gln Ile Asp Gly Ile Ile Ile Ser Ser
 50 55 60
 gta gtg cgg cca atc atg ttt ggg tta gaa aga atg tgg aca aaa taa 240
 Val Val Pro Pro Ile Met Phe Ala Leu Glu Arg Met Cys Thr Lys Tyr
 65 70 75 80
 ttt cat atc gaa cct caa att gtt ggt caa ggt ata aaa atc tat tta 288
 Phe His Ile Gln Pro Gln Ile Val Gly Pro Gly Met Lys Thr Gly Leu
 85 90 95
 tat ata aaa ttt gat aat cgg aaa gaa gta ggg aca gac ata atc ata 336
 Asn Ile Lys Tyr Asp Asn Pro Lys Gln Val Gly Ala Asp Arg Ile Val
 100 105 110
 tat ttt ttt ttt ttt ata gat ttt tat ttt gat tta att ttt ttt 384
 Asn Ala Val Ala Ala Ile His Leu Tyr Gly Asn Pro Leu Ile Val Val
 115 120 125
 tat ttt ttt att gtt att att tat ttt tat att tat tta att tta 432
 Asn Ile Gly Thr Ala Thr Thr Tyr Tyr Tyr Ile Asp Glu Asn Lys Val
 130 135 140

tac atg ggc ggc ggc att gcc cct ggg att aca att tgg aca gag ggc 480
Tyr Met Gly Gly Ala Ile Ala Pro Gly Ile Thr Ile Ser Thr Glu Ala
145 150 155 160

ctt tac tgg cgt gca gca aag ctt cct cgt atc gaa atc acc cgg ccc 528
Leu Tyr Ser Arg Ala Ala Lys Leu Pro Arg Ile Glu Ile Thr Arg Pro
165 170 175

gac aat att atc gga aaa aac att gtt agc gag atg caa tct gga att 576
Asp Asn Ile Ile Gly Lys Asn Thr Val Ser Ala Met Gln Ser Gly Ile
180 185 190

tta ttt ggc tat gtc ggc caa gtg gaa gga atc gtt aag cga atg aaa 624
Leu Phe Gly Tyr Val Gly Gln Val Glu Gly Ile Val Lys Arg Met Lys
195 200 205

tgg cag gca aaa cag gac cca agg tca ttg cga cag gag gcc tgg cgt 672
Trp Gln Ala Lys Gln Asp Pro Arg Ser Leu Arg Gln Glu Ala Trp Arg
210 215 220

cgc tca ttg cga acg aat cag att gta tag 702
Arg Ser Leu Arg Thr Asn Gln Ile Val
225 230

<210> +5

<211> 233

<212> PRT

<213> Bacillus subtilis

<400> +5

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Tyr His Asp Gly Lys Leu Glu Tyr His Trp Arg Ile Glu Thr Ser Arg
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His Lys Thr Glu Asp Glu Phe Gly Met Ile Leu Arg Ser Leu Phe Asp
35 40 45

His Ser Gly Leu Met Phe Glu Gln Ile Asp Gly Ile Ile Ile Ser Ser
50 55 60

Val Val Pro Pro Ile Met Phe Ala Leu Glu Arg Met Cys Thr Lys Tyr
65 70 75 80

Phe His Ile Glu Pro Gln Ile Val Gly Pro Gly Met Lys Thr Gly Leu
85 90 95

Asn Ile Lys Tyr Asp Asn Pro Lys Glu Val Gly Ala Asp Arg Ile Val
100 105 110

Asn Ala Val Ala Ala Ile His Leu Tyr Gly Asn Pro Leu Ile Val Val
115 120 125

Asp Phe Gly Thr Ala Thr Thr Tyr Cys Tyr Ile Asp Ala Asn Lys His
130 135 140

Tyr Met Gly Gly Ala Ile Ala Trp Gly Ile Thr Ile Ser Thr Glu Ala
145 150 155 160

Leu Tyr Ser Arg Ala Ala Lys Leu Pro Arg Ile Glu Ile Thr Arg Pro
 165 170 175

Asp Asn Ile Ile Gly Lys Asn Thr Val Ser Ala Met Gln Ser Gly Ile
 180 185 190

Leu Phe Gly Tyr Val Gly Gln Val Glu Gly Ile Val Lys Arg Met Lys
 195 200 205

Trp Gln Ala Lys Gln Asp Pro Arg Ser Leu Arg Gln Glu Ala Trp Arg
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Arg Ser Leu Arg Thr Asn Gln Ile Val
 225 230

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<211> 1623

<212> DNA

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<221> CDS

<222> (1)..(1620)

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tac aag ata aag gac ctg aaa tta tgg ttg ccc ggc acg aac aac acg 96
 Tyr Lys Ile Lys Asp Leu Lys Leu Ser Leu Pro Gly Thr Asn Lys Thr
 20 25 30

cag caa ttc atg ggc caa gaa gtc ggt cgt tta act gga aac ccc gga 144
 Gln Gln Phe Met Ala Gln Ala Val Gly Arg Leu Thr Gly Lys Pro Gly
 35 40 45

gtg gtg tta ctg aca tca gga cag ggt gac cct aac tta aca aca ggc 192
 Val Val Leu Val Thr Ser Gly Pro Gly Ala Ser Asn Leu Ala Thr Gly
 50 55 60

ctg ctg aca gag aac act gaa gga gac cct gtc gtt gag ctt got gga 240
 Leu Leu Thr Ala Asn Thr Glu Gly Asp Pro Val Val Ala Leu Ala Gly
 65 70 75 80

aac gtg atc ctt tca tct cgt tta aaa ccc aca cat aac tct tta tat 288
 Asn Val Ile Arg Ala Tyr Arg Leu Lys Arg Thr His Gln Ser Leu Asp
 85 90 95

aac cag ggt tta ttc caa cag att aca aca tca act tta aac gtt caa 336
 Asn Ala Ala Leu Phe Gln Pro Ile Thr Lys Tyr Ser Val Gln Val Gln
 100 105 110 115

cat tta aaa atc ata cct tta cct cct aca cat cct tta cct atc atc 384
 Asp Val Lys Asn Ile Pro Glu Ala Val Thr Asn Ala Ile Arg Ile Ala
 120 125 130 135

tca tca ttt cct att gtt ctt ctt ttt cgt cgt ttt cct tca ttt ttt 432
 Ser Ala Gly Phe Ala Gly Ala Ala Phe Val Ser Phe Phe Glu Arg Val
 140 145 150 155

gtg aat gaa gtc aca aat atg aaa aac gtg agt gat gtt gca gag cca Val Asn Glu Val Thr Asn Thr Lys Asn Val Arg Ala Val Ala Ala Pro 145 151 155 161	480
aaa ctc ggt cct gca gca gat gat gca atc agt gag gac ata gca aaa Lys Leu Gly Pro Ala Ala Asp Asp Ala Ile Ser Ala Ala Ile Ala Lys 165 170 175	528
atc caa aca gca aaa ctt cct gtc gat ttg gtc ggc atg aaa ggc gga Ile Gln Thr Ala Lys Leu Pro Val Val Leu Val Gly Met Lys Gly Gly 180 185 190	576
aga cag gaa gga att aaa gag gtt agc aag ctt ttg aaa aag gtt cag Arg Pro Glu Ala Ile Lys Ala Val Arg Lys Leu Leu Lys Lys Val Gln 195 200 205	624
ctt cca ttt gtt gaa aca tat caa got got ggt acc ctt tct aga gat Leu Pro Phe Val Glu Thr Tyr Gln Ala Ala Gly Thr Leu Ser Arg Asp 210 215 220	672
tta gag gat caa tat ttt ggc agt atc ggt ttg ttc agc aac cag cct Leu Glu Asp Gln Tyr Phe Gly Arg Ile Gly Leu Phe Arg Asn Gln Pro 225 230 235 240	720
ggc gat tta atg cta gag cag gca gat gtt gtt ttg aag atc ggc tat Gly Asp Leu Leu Leu Glu Gln Ala Asp Val Val Leu Thr Ile Gly Tyr 245 250 255	768
gac cag att gaa tat gat cag aaa ttc tgg aat atc aat gaa gac cag Asp Pro Ile Glu Tyr Asp Pro Lys Phe Trp Asn Ile Asn Gly Asp Arg 260 265 270	816
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caa cct gat ctt gaa ttg atc ggt gac att cag ttc aag atc aat cat His Pro Asp Leu Glu Leu Ile Gly Asp Ile Pro Ser Thr Ile Asn His 290 295 300	912
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ttt ctt tct cat tta aaa caa tat atg cat gaa gat gag cag gtt ctt Ile Leu Ser Asp Leu Lys Gln Tyr Met His Glu Gly Gln Gln Val Pro 325 330 335	1008
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 Thr Leu Met Ile Ser Asn Gly Met Gln Thr Leu Gly Val Ala Leu Pro
 388 390 395 400

tgg gga atc ggc gct tca ttg gtg aaa cag gga gaa aaa gtg gtt tat 1248
 Trp Ala Ile Gly Ala Ser Leu Val Lys Pro Gly Ala Lys Val Val Ser
 405 410 415

gtc ttc ggt gac ggc ggt ttc tta tta tca gca atg gaa tta gag ata 1286
 Val Ser Gly Asp Gly Gly Phe Leu Phe Ser Ala Met Glu Leu Glu Thr
 420 425 430

gca gtt cga cta aaa gca cca atc gta cac att gta tgg aac gac ago 1344
 Ala Val Arg Leu Lys Ala Pro Ile Val His Ile Val Trp Asn Asp Ser
 435 440 445

aca tat gac atg ttg aat ttc cag aca ttg aaa aca tat aac gtt ata 1380
 Thr Tyr Asp Met Val His Phe Gln Gln Leu Lys Lys Tyr Asn Arg Thr
 450 455 460

tct ggc gtc gat ttc gga aat atc gat atc gtg aaa tat ggc gaa ago 1440
 Ser Ala Val Asp Phe Gly Asn Ile Asp Ile Val Lys Tyr Ala Glu Ser
 465 470 475

ttc gga gaa acg ggc ttg cgc gta gaa tca cca gac cag ctg gca gat 1488
 Phe Gly Ala Thr Ala Leu Arg Val Glu Ser Pro Asp Gln Leu Ala Asp
 485 490 495

gtt atc cgt caa ggc atg aac gct gaa ggt cct gtc atc atc gat gtc 1536
 Val Leu Arg Gln Gly Met Asn Ala Glu Gly Pro Val Ile Ile Asp Val
 500 505 510

cca gtt gac tac att gat aac att aat tta gca gtt gac aac att cca 1584
 Pro Val Asp Tyr Ser Asp Asn Ile Asn Leu Ala Ser Asp Lys Leu Pro
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<211> 840

<212> 887

<213> Bacillus subtilis

<400> 87

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Tyr Lys Ile Lys Asp Leu Lys Leu Ser Leu Pro Gly Thr Asn Lys Thr
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Gln Gln Phe Met Ala Gln Ala Val Gly Arg Leu Thr Gly Lys Pro Gly
 35 40 45

Val Val Leu Val Thr Ser Gly Pro Gly Ala Ser Asn Leu Ala Thr Gly
 50 55 60

Leu Leu Thr Ala Asn Thr Gln Gly Asp Pro Val Val Ala Leu Ala Gly
 65 70 75

Asn Val Ile Arg Ala Tyr Arg Leu Lys Arg Thr His Gln Ser Leu Asp
 85 90 95
 Asn Ala Ala Leu Phe Gln Pro Ile Thr Lys Tyr Ser Val Gln Val Gln
 100 105 110
 Asp Val Lys Asn Ile Pro Gln Ala Val Thr Asn Ala Phe Arg Ile Ala
 115 120 125
 Ser Ala Gly Gln Ala Gly Ala Ala Phe Val Ser Phe Pro Gln Asp Val
 130 135 140
 Val Asn Gln Val Thr Asn Thr Lys Asn Val Arg Ala Val Ala Ala Pro
 145 150 155 160
 Lys Leu Gly Pro Ala Ala Asp Asp Ala Ile Ser Ala Ala Ile Ala Lys
 165 170 175
 Ile Gln Thr Ala Lys Leu Pro Val Val Leu Val Gly Met Lys Gly Gly
 180 185 190
 Arg Pro Gln Ala Ile Lys Ala Val Arg Lys Leu Leu Lys Lys Val Gln
 195 200 205
 Leu Pro Phe Val Gln Thr Tyr Gln Ala Ala Gly Thr Leu Ser Arg Asp
 210 215 220
 Leu Gln Asp Gln Tyr Phe Gly Arg Ile Gly Leu Phe Arg Asn Gln Pro
 225 230 235 240
 Gly Asp Leu Leu Leu Ala Gln Ala Asp Val Val Leu Thr Ile Gly Tyr
 245 250 255
 Asp Pro Ile Gln Tyr Asp Pro Lys Phe Trp Asn Ile Asn Gly Asp Arg
 260 265 270
 Thr Ile Ile His Leu Asp Gln Ile Ile Ala Asp Ile Asp His Ala Tyr
 275 280 285
 Gln Pro Asp Leu Gln Leu Ile Gly Asp Ile Pro Ser Thr Ile Asn His
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 Ile Gln His Asp Ala Val Lys Val Gln Phe Ala Gln Arg Gln Gln Lys
 305 310 315 320
 Ile Leu Ser Asp Leu Lys Gln Tyr Met His Gln Gly Gln Gln Val Pro
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 Ala Asp Trp Lys Ser Asp Arg Ala His Pro Leu Gln Ile Val Lys Gln
 340 345 350 355
 Leu Arg Asn Ala Val Asp Asp His Val Thr Val Thr Lys Asp Ile Gly
 360 365 370
 Ser His Ser Ile Trp Met Ser Arg Tyr Phe Arg Ser Tyr Ala Pro Leu
 375 380 385
 Thr Leu Met Ile Ser Asn Gly Met Gln Thr Leu Gly Val Ala Leu Ile
 390 395 400

Trp Ala Ile Gly Ala Ser Leu Val Lys Pro Gly Glu Lys Val Val Ser
 405 410 415
 Val Ser Gly Asp Gly Gly Phe Leu Phe Ser Ala Met Glu Leu Glu Thr
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 Ala Val Arg Leu Lys Ala Pro Ile Val His Ile Val Trp Asn Asp Ser
 435 440 445
 Thr Tyr Asp Met Val His Phe Gln Gln Leu Lys Lys Tyr Asn Arg Thr
 450 455 460
 Ser Ala Val Asp Phe Gly Asn Ile Asp Ile Val Lys Tyr Ala Glu Ser
 465 470 475 480
 Phe Gly Ala Thr Ala Leu Arg Val Glu Ser Pro Asp Gln Leu Ala Asp
 485 490 495
 Val Leu Arg Gln Gly Met Asn Ala Glu Gly Pro Val Ile Ile Asp Val
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<211> 23

<212> CNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: ribosome
binding site

<220>

<221> misc-feature

<222> 14-23

<223> n = a, c, g, or t

<400> 54

agaaaggagg tgaannnnnn atg

23

<210> 44

<211> 7

<212> FRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: 1an'
terminus

<400> 44

ile arg ala met glu arg ile

<210> 44

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 C terminus

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<210> 91
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 <213> Artificial Sequence

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 C terminus

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 1 5

<210> 92
 <211> 6695
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 <213> Artificial Sequence

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 pAN33c plasmid

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 aaaaaattg atgcctgga catcgaaa agcgggac gtaaatat tgaacggt 360
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